

Fig. 1A

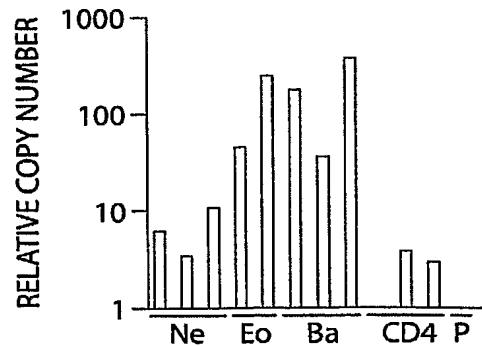


Fig. 1B

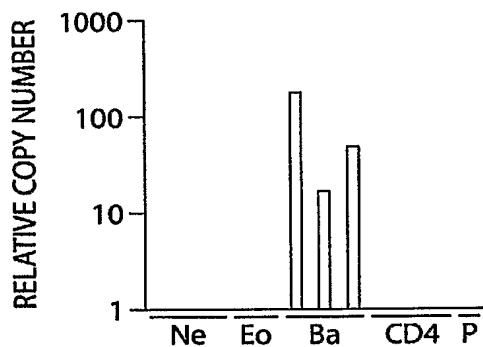


Fig. 1C

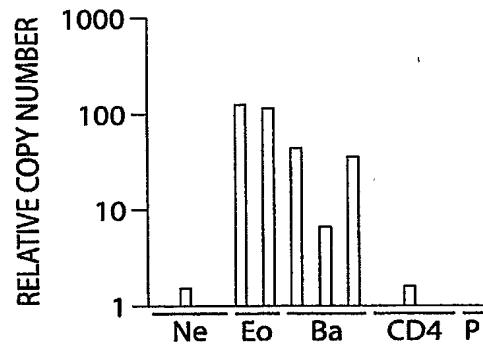


Fig. 1D

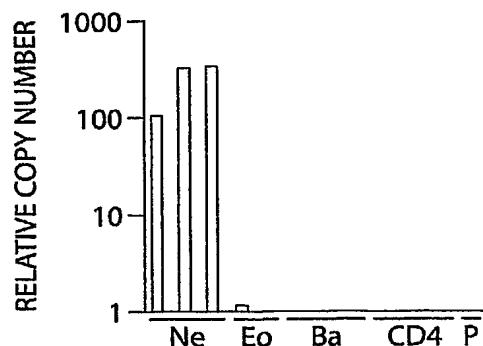


Fig. 1E

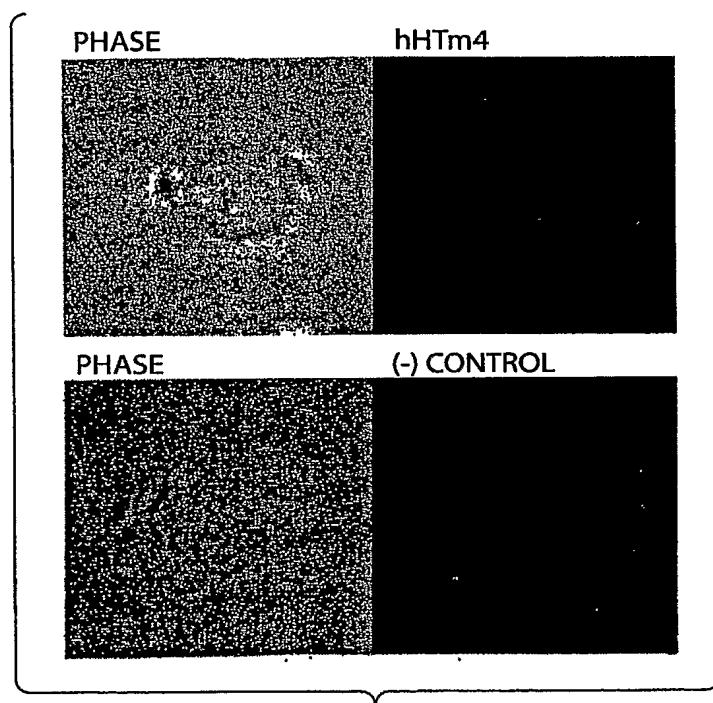


Fig. 2

Figure 3. Granulocyte subtype-specific transcripts for ion channels and receptors

<u><b>Ion Channels</b></u>	<u><b>Ion Channel Transcript (Accession #, GenBank)</b></u>	<u><b>Cell-type<sup>a</sup></b></u>	<u><b>MC</b></u>	<u><b>Ba</b></u>	<u><b>Eo</b></u>	<u><b>Ne</b></u>	<u><b>PI</b></u>	<u><b>CD4</b></u>	<u><b>CD8</b></u>	<u><b>CD14</b></u>	<u><b>CD19</b></u>	<u><b>Fb</b></u>	<u><b>TC<sup>b</sup></b></u>	<u><b>Gene Functions</b></u>
<u><b>Ca<sup>2+</sup> channel type A1 D (BE550599) aquaporin 9 (NM_020980) 602914</b></u>		Ba, Eo Ne	0.1 0.7	1.7 0.1	1.5 0.4	0.4 137.4	0.0 0.9	0.3 0.1	0.1 8.6	0.0 0.1	0.3 0.1	0.0 0.2	0.0 0.2	facilitates uptake of the metalloids arsenite and antimonite
<u><b>K<sup>+</sup> channel Kir 1.3 (U73191) 600359</b></u>		Ne	0.9	0.2	0.4	99.5	0.7	0.2	0.0	0.8	0.0	0.0	5	Andersen syndrome (170390) and Barter syndrome (241200)
<u><b>K<sup>+</sup> channel Kir 2.1 (AF153820) 600681</b></u>		Ne	0.7	3.8	5.3	40.7	0.4	0.2	0.5	1.5	0.7	1.1	6	Andersen syndrome (170390) and Barter syndrome (241200)
<u><b>GPCR histamine H<sub>4</sub> R (AF312230) 606792</b></u>		Ba	0.7	34.2	9.4	0.7	0.4	0.8	0.5	0.6	0.0	0.1	0	expression of HRH4 conferred sensitivity
<u><b>PGC<sup>c</sup> R type 3a2] (X83858) 176806</b></u>		Ba, Eo	0.8	10.3	0.1	0.7	0.6	0.3	0.2	0.2	0.5	1.7	0	signaling pathways
<u><b>C3aR (U62077) 605246</b></u>		Ba, Eo	11.8	55.7	39.4	2.0	1.6	1.6	1.5	3.0	0.6	0.5	3	anaphylatoxin receptor importance for eosinophil responses
<u><b>CCR3 (NM_001837) 601268</b></u>		Ba, Eo	0.6	117.4	90.9	24.9	0.2	0.5	0.4	0.2	0.2	0.4	0	mediate signals to the interior of the cell via activation of heterotrimeric G proteins
<u><b>CRTH2 (NM_004778) 604837</b></u>		Ba, Eo	1.1	26.0	38.2	2.0	0.8	1.4	1.0	1.2	0.9	0.5	0	Probably involved in cellular response to a hormone
<u><b>EMR-1 (NM_001974) 600493</b></u>		Ba, Eo	0.8	33.5	90.9	4.2	3.4	1.7	0.8	7.1	1.6	0.5	1	cardioprotective function P2RY2 may participate in control of the cell cycle of endometrial carcinoma cells
<u><b>adenosine A<sub>3</sub> R (NM_000677) 600445</b></u>		Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5	0	GPR105 is a G-protein-coupled receptor identifying a quiescent, primitive population of hematopoietic cells restricted to bone marrow. GPR105 might play an important role in peripheral and neuroimmune function
<u><b>P2Y2 purinergic R (NM_002564) 600041</b></u>		Eo	0.1	0.1	5.5	0.1	0.2	0.1	0.3	1.2	0.2	0.1	0	edg-4 mRNA was expressed in mouse islets; edg-4 (lpa2) r is a distinctive functional marker for ovarian carcinoma and is expressed both as the wild-type and a carboxy-terminally extended gain-of-function mutant. the highest levels of gpr43 were
<u><b>GPR, Edg-4 (AF011466) 605110</b></u>		Eo, Ne	1.3	2.8	15.9	24.2	0.1	3.6	5.0	3.8	1.9	0.9	2	
<u><b>PAR1-like GPR43 (NM_005306)</b></u>		Eo, Ne	0.3	0.7	12.4	35.2	0.8	0.1	0.1	0.7	0.4	0.1	0	

603823	C5aR (NM_001736) 113995	Ne	2.3	21.6	13.6	92.6	2.3	1.2	0.5	25.6	1.0	0.4	5
	CXCR1 IL-8R (NM_000634) 146929	Ne	0.2	4.3	0.3	83.4	0.4	0.3	0.2	0.2	0.1	0.1	0
	CXCR2 IL-8R (NM_001557)	Ne	0.2	1.1	1.5	112.1	2.7	0.3	0.8	0.7	0.6	0.0	1
	formyl peptide R 1 (NM_002029) 136537	Ne	2.8	23.5	8.8	282.9	3.6	1.3	0.7	62.6	1.1	0.5	0

found in immune cells; gpi43 is highly restricted in hematopoietic tissues, receptor for the chemotactic and inflammatory peptide anaphylatoxin C5a. this receptor stimulates chemotaxis, granule enzyme release and superoxide anion production.

receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to mgsa (gro) with a low affinity.

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HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED

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## Fig. 3C

VIA A G-PROTEIN THAT ACTIVATES PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.									
<u>likely FPR2 mediates superoxide production at high concentrations of FMLF</u>									
formyl peptide R 2 ( <u>U81501</u> )	Ne	0.4	0.5	0.6	75.5	0.1	1.0	0.6	6.0
GPR77 ( <u>NM_018485</u> )	Ne	0.1	0.9	0.8	3.4	0.0	0.3	0.2	1.0
GPR86 purinergic R ( <u>NM_023914</u> )	Ne	0.3	0.2	17.9	882	1.9	0.1	0.2	12.3
PAR2 (BEE953369) <u>600933</u>	Ne	0.1	0.3	2.2	36.2	0.1	0.7	0.1	1.6
Other Receptors									
Fc ε RI α ( <u>BC005912</u> ) <u>147138</u>	Ba	19.4	219.0	4.6	5.5	1.4	5.1	0.8	1.4
<u>HTmr4</u> ( <u>35848</u> ) <u>606498</u>	Ba	0.6	133.1	6.9	3.5	0.2	0.5	0.4	0.1
IL-3 R ( <u>NM_002183</u> ) <u>3008385</u>	Ba	0.6	52.6	2.0	0.7	0.2	0.3	0.2	0.7
CD244 NK cell R <u>NM_016382</u> <u>605554</u>	Ba, Eo	0.3	56.0	16.5	1.2	0.1	0.4	3.5	5.2
fibroblast growth factor R 2 ( <u>NM_022969</u> ) <u>176943</u> <u>IL-5R α (M759-4)</u> <u>147851</u>	Ba, Eo	0.1	27.9	12.1	0.2	0.1	0.1	0.2	0.1
Siglec 8 ( <u>NM_014442</u> ) <u>605639</u>	Eo	1.8	0.3	17.4	0.4	0.3	0.2	0.1	0.2
CD117 c-KIT ( <u>NM_000222</u> ) <u>164920</u>	MC	89.0	7.2	4.2	1.2	0.8	0.2	0.5	0.1
SiglecB D86358 <u>604405</u>	MC	5.6	0.2	0.0	0.2	0.5	0.0	0.0	0.4
Fc ε RΙ $\beta$ ( <u>NM_000139</u> ) <u>147138</u> <u>low density lipoprotein R</u>	MC, Ba	22.3	44.3	0.4	0.6	1.6	0.5	0.2	0.0
	MC, Ba	20.7	20.4	1.3	1.8	2.3	2.1	3.4	3.5
								0.8	0.8
								6.3	6.3
								0	0
								0.1	0.1
								34	34

<u>(NM_000527) 606945</u> <u>TRK neurotrophin R (NM_002529)</u> <u>191315</u>	Mc, Ba	4.6	7.3	0.1	0.1	0.1	0.1	0.0	0.0	0	0.0	0
<u>butyrophilin like R (AK025267)</u>	Ne	1.1	1.7	1.5	6.9	1.5	1.7	1.6	0.9	1.5	1.3	1
<u>CD120a, TNF-R-1 (NM_001065)</u> <u>191190</u>	Ne	1.7	1.2	7.8	74.7	1.3	2.2	5.9	17.4	0.6	16	35

participates in the primary signal transduction mechanism of NGF; is also an immunoregulatory cytokine acting on monocytes. His gene is mainly expressed in small intestine, colon, testis, and leukocytes. Receptor for TNFSE2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Contributes to the induction of noncytotoxic TNF-effects including anti-viral state and activation of the acid sphingomyelinase. Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance in the antigen-stimulated suicide of mature T-cells, or both. The secreted

Fig. 3D

<i>decoy R1, TRAILR3 (AF012536) 603613</i>	Ne	0.1	1.5	7.7	78.7	0.5	0.2	0.1	0.7	0.1	0.6	0
<i>FCy R IIC2 (U90939) FCy R IIC3 (U90940) FCy R III (J04162) 146740</i>	Ne	1.5	2.4	7.8	59.9	0.3	0.2	0.1	7.2	2.3	0.2	2
Ne	2.4	10.7	10.0	84.3	3.0	1.4	0.6	0.6	14.0	7.2	1.0	5
Ne	0.7	1.6	1.9	199.6	6.6	1.3	1.3	2.2	2.6	0.1	4	
<i>G-CSFR (NM_0007601) 138971</i>	Ne	0.1	0.4	1.6	163.6	0.2	0.8	0.2	25.5	0.1	0.2	3
<i>IL-13 R (U81379) 308385</i>	Ne	0.3	0.2	2.0	14.1	0.4	0.4	0.3	2.9	1.3	1.3	0
<i>IL-1R, type II (NM_004633) 147811</i>	Ne	0.1	0.1	0.1	53.5	0.2	0.4	0.1	0.2	0.0	0.0	3
<i>IGFR 1 (NM_000875) 147370</i>	Ne	0.3	3.5	5.0	17.4	1.6	0.1	2.8	2.4	2.0	3.5	3
<i>IGFR 2 (NM_000876) 147280</i>	Ne	4.6	0.9	5.4	85.3	1.7	2.9	8.7	8.4	4.8	15	32
<i>leukocyte immunoglobulin-like RA2 (NM_006866) 604812</i>	Ne	0.5	5.8	4.3	41.2	1.8	0.0	0.1	11.6	0.5	0.1	2
<i>Toll-like R 1 (AL050262) 601194</i>	Ne	0.6	0.3	1.2	31.5	1.6	0.8	0.7	3.0	1.5	0.3	0
<i>Toll-like R 2 (NM_003264) 603028</i>	Ne	0.9	6.0	1.3	83.8	1.6	1.3	0.1	26.3	0.9	0.4	0
<i>Toll-like R 6 (NM_006068)</i>	Ne	0.5	1.0	0.9	8.8	0.1	0.9	0.9	2.1	1.2	0.6	0

a. Cell-type specificity was obtained by comparing the "normalized AD" levels of each gene in mast cells (MC; average of 2 experiments), basophils (Ba; average of 3 experiments), eosinophils (Eo; average of 4 experiments), neutrophils (Ne; average of 4 experiments), platelets (Pl), CD4<sup>+</sup> cells (CD4), CD8<sup>+</sup> cells (CD8), CD14<sup>+</sup> cells (CD14), CD19<sup>+</sup> cells (CD19) and nasal polyp-derived cultured fibroblasts (Fb).

Fig. 3E

	CB cultured MCs	Basophils	cultured basophils	Eosinophils	Neutrophils	platelets	Erythrocytes	CD4	CD8	CD14	CD19
Spink5	21	17	11	22	16	30	15	28	36	129	104
chymase human	1221	47	65	45	12	101	62	108	59	104	45
tryptase alpha	21179	212	40	33	25	184	139	104	17	52	39
tryptase beta	25414	195	113	49	28	152	10	122	113	93	6
tryptase delta	349	45	6	23	55	74	113	11	10	42	11
tryptase gamma	654	56	19	38	78	28	24	81	230	142	83
TRPV2	129	37	15	97	99	259	137	133	67	97	110
ANKTM1_-	28	28	8	38	30	96	18	14	46	11	28
Cannabinoid receptor type 1	50	41	14	47	36	27	61	41	56	18	54
Cannabinoid receptor type 2	160	369	226	578	177	271	530	324	232	212	421

Fig. 4A

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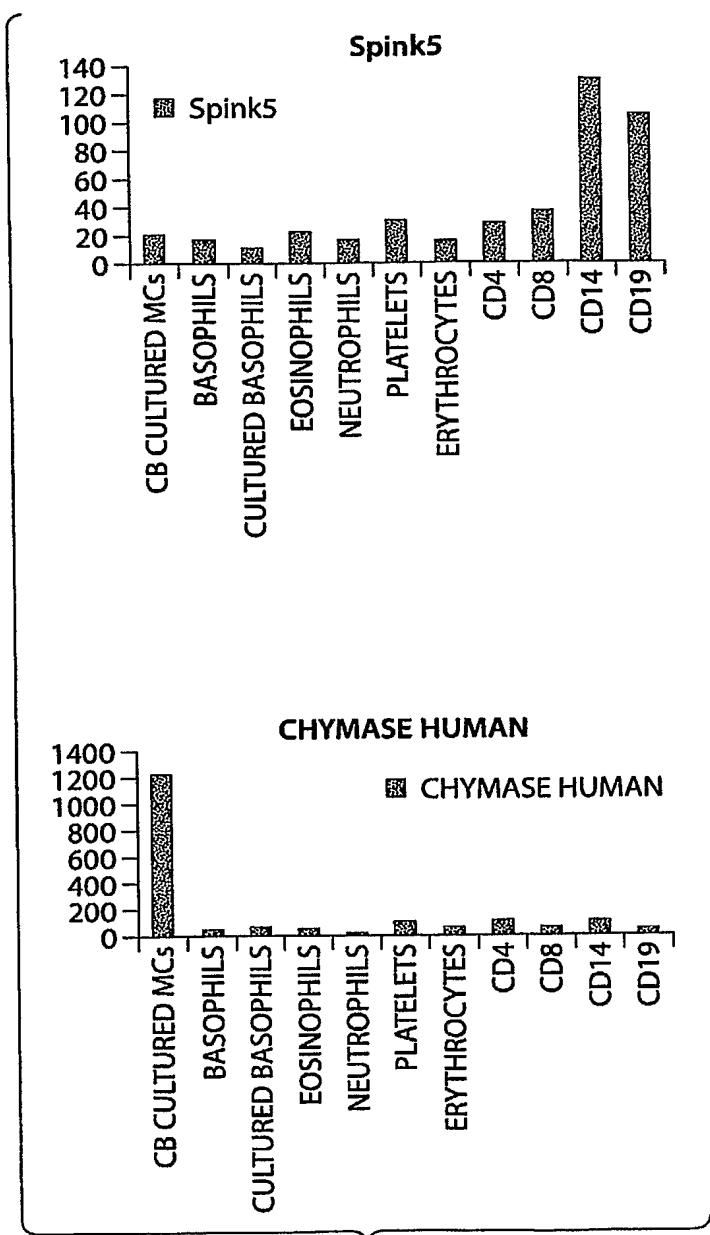


Fig. 4B

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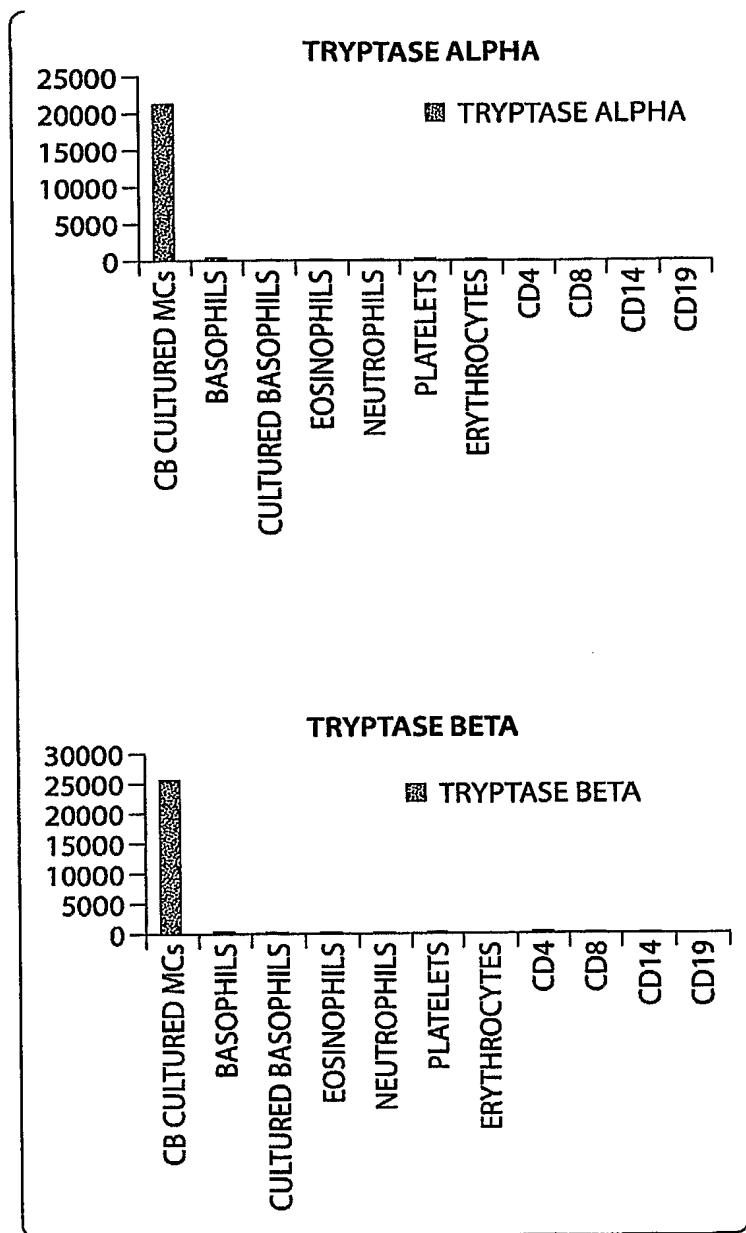


Fig. 4C

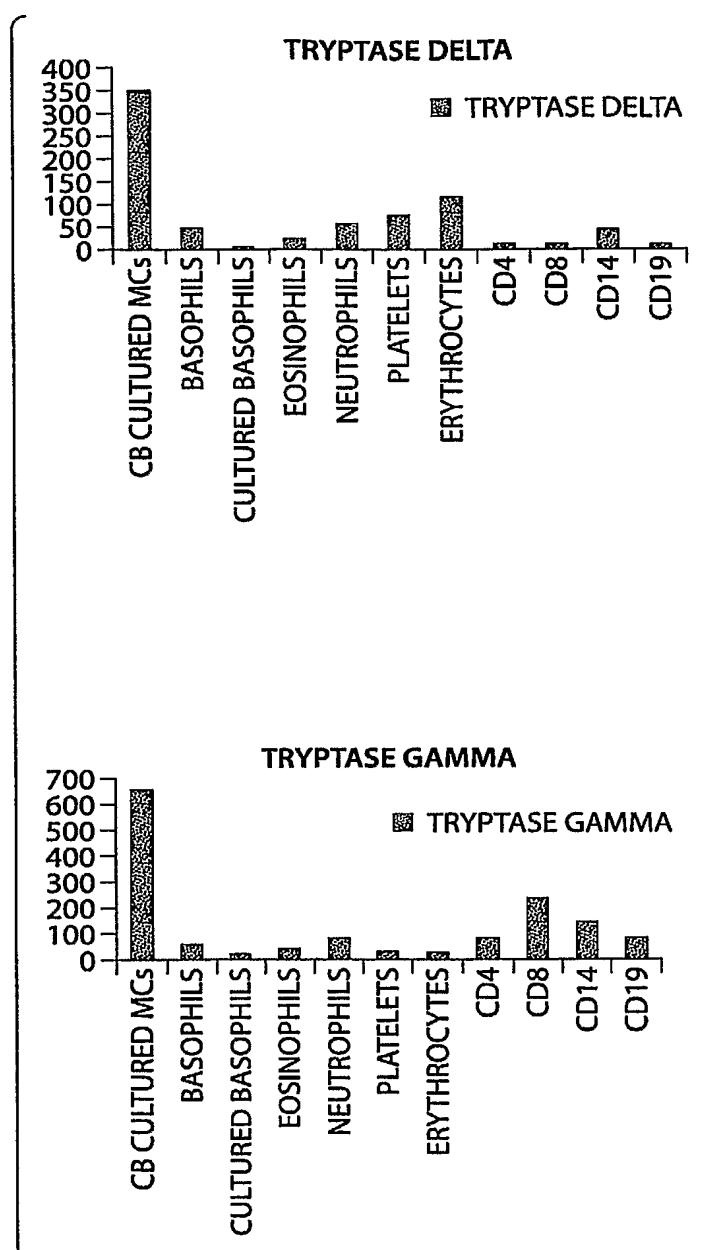


Fig. 4D

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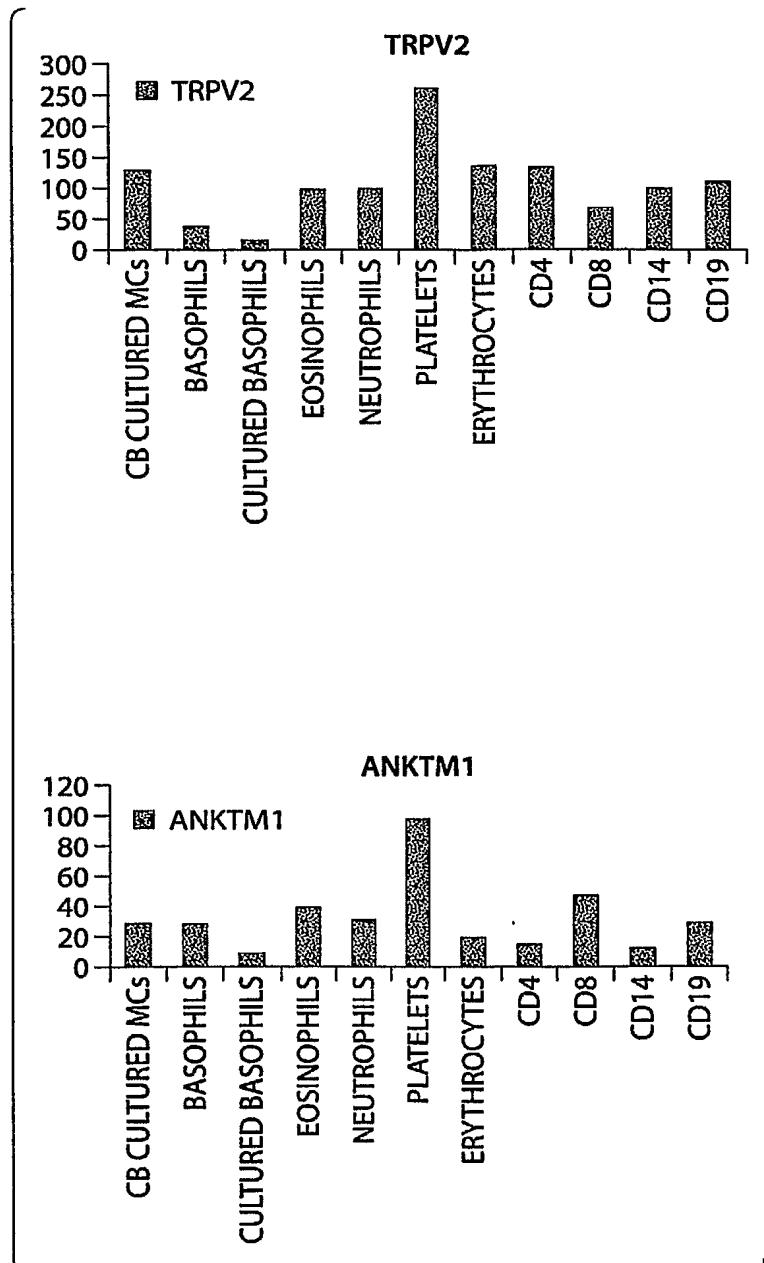


Fig. 4E

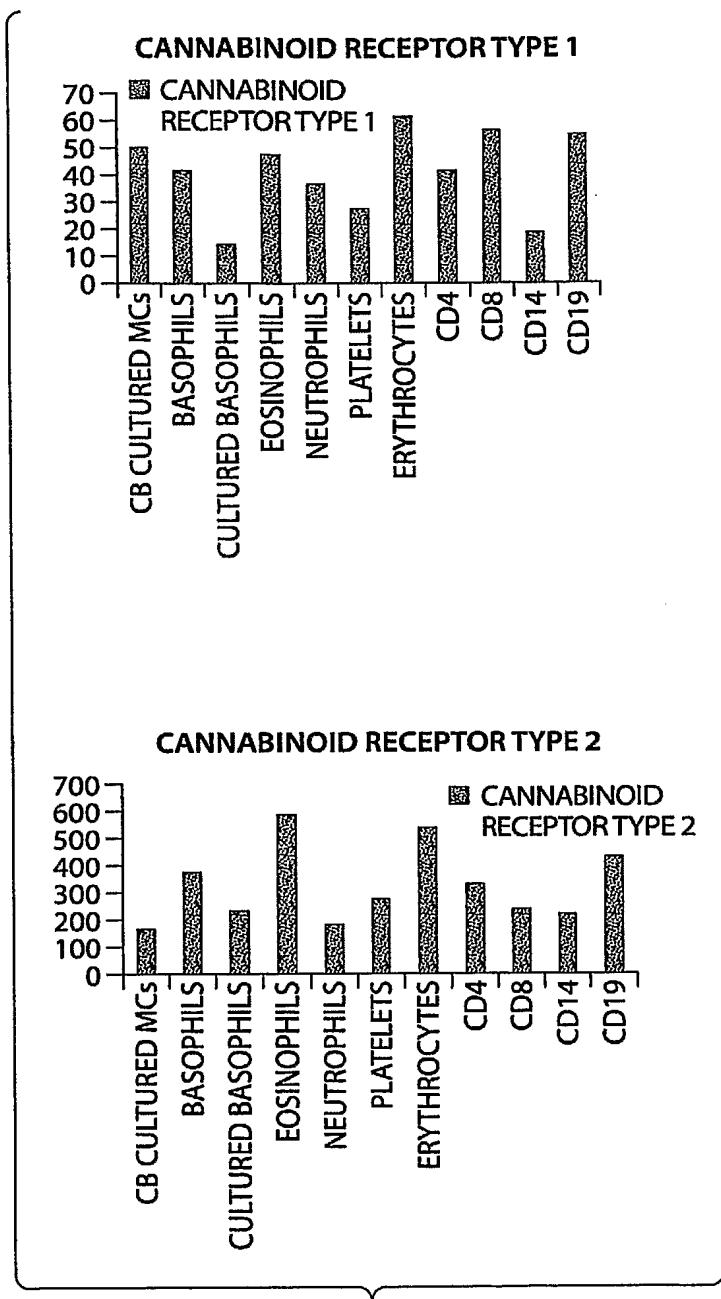


Fig. 4F

Fig. 5A

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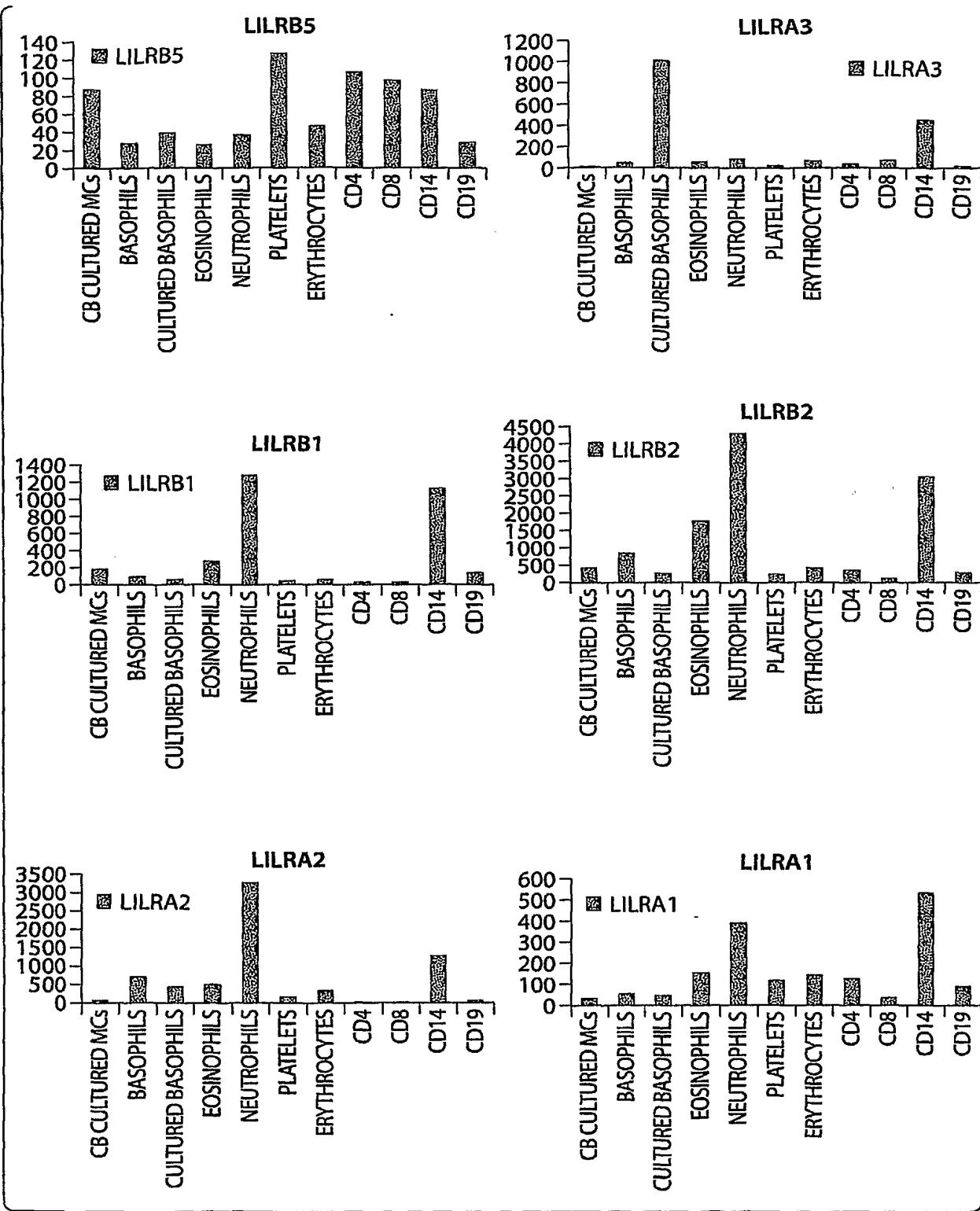


Fig. 5B

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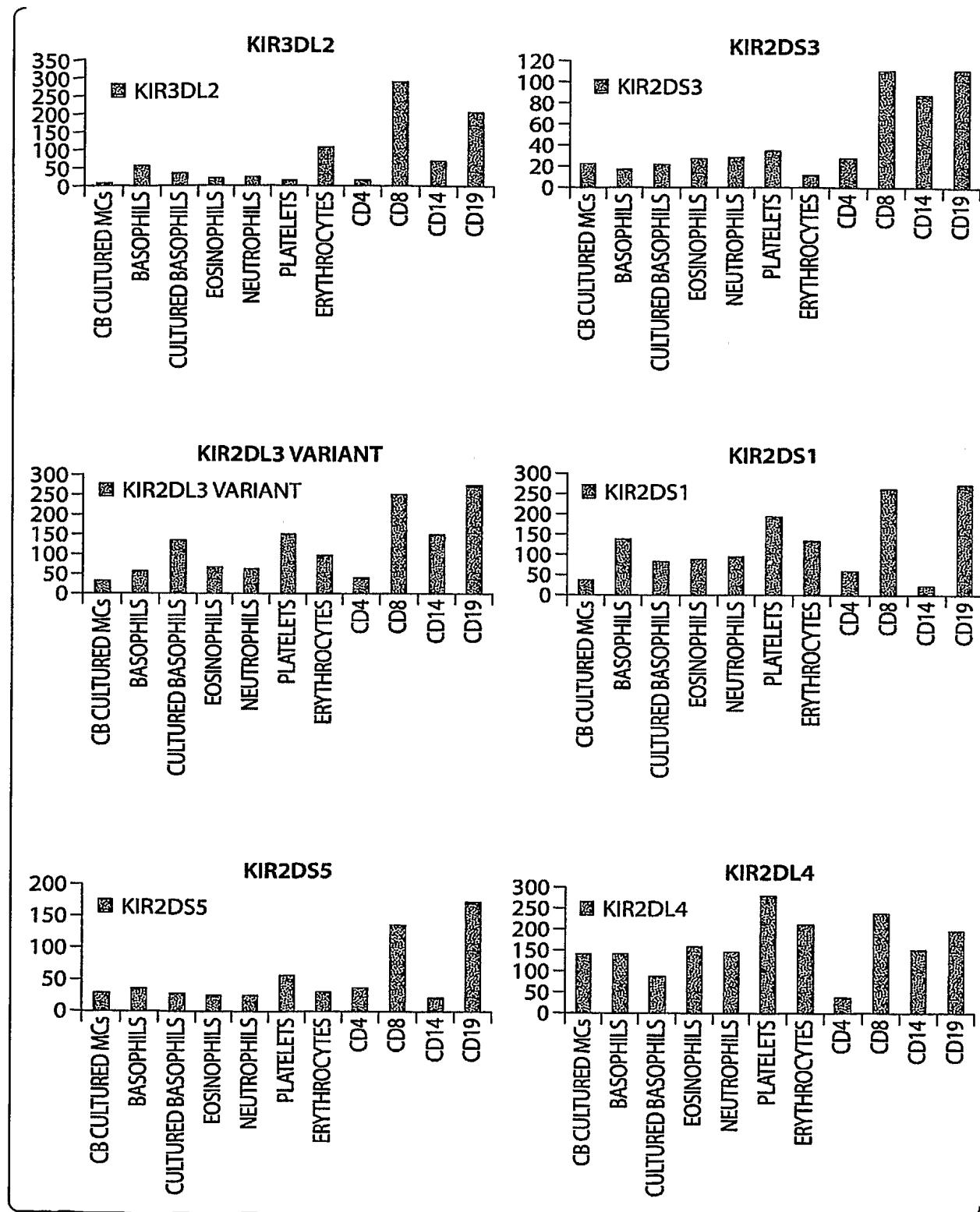


Fig. 5C

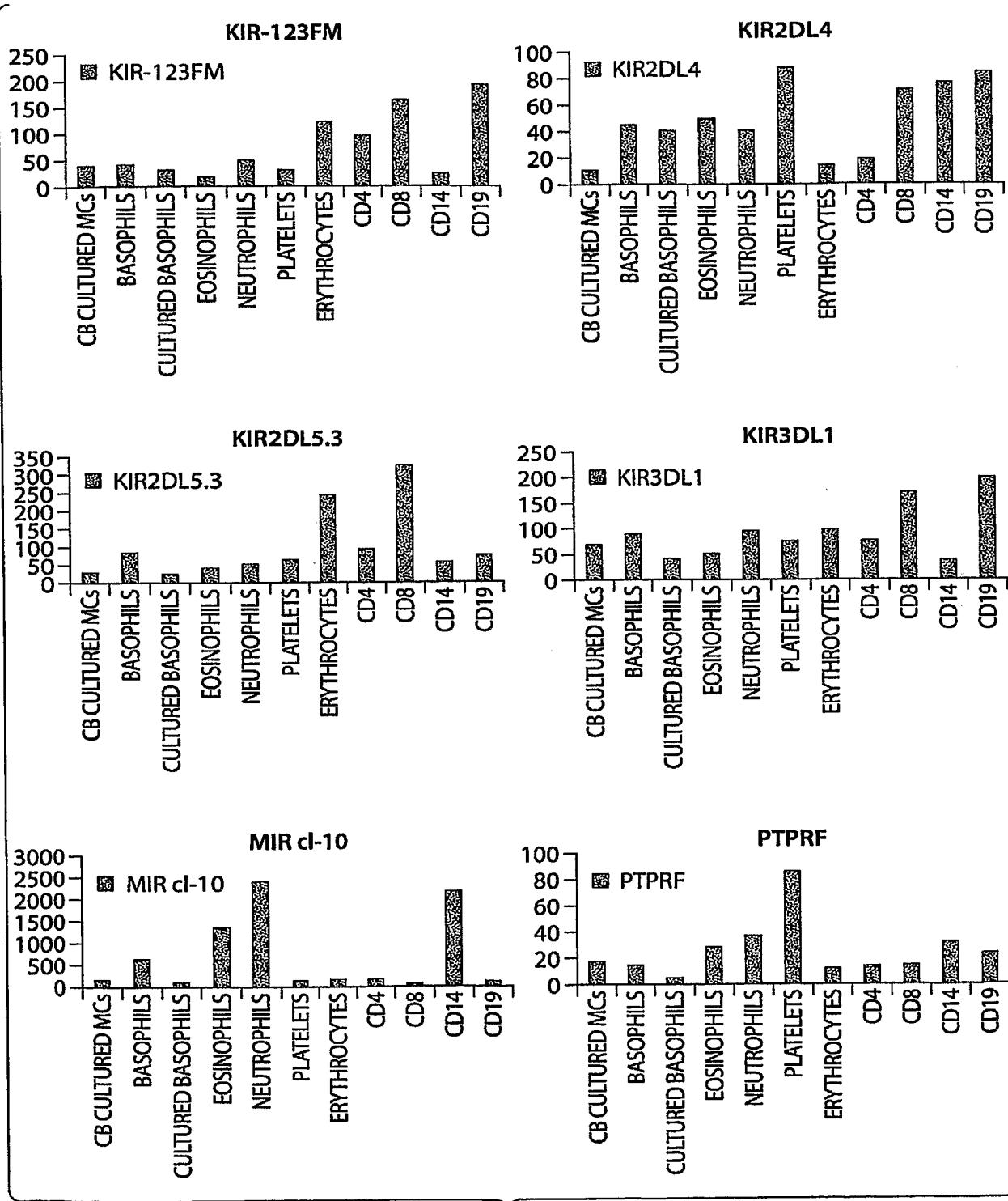


Fig. 5D

Table E1. The complete list of granulocyte subtype-selective transcripts. Selectivity index (S.I.) was calculated by comparing the "normalized AD" level of a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types including platelets (Pl), CD4<sup>+</sup> cells, CD14<sup>+</sup> cells, CD19<sup>+</sup> cells and nasal polyp-derived cultured fibroblasts (Fb). When the result was accompanied by presence call, it was shown as a bold numeral. Italic numerals show that the raw AD levels were associated with absence call by the GeneChip analysis software. Transcripts having S.I. >3-fold were shown in A-H. Abbreviations used in the table through A-I were (small); the results obtained by the small sample protocol (see materials and methods), R: receptor, and ICN: ion channel.

A. Basophil (Ba)-selective transcripts (1/2).

Probe set	Accession #	Transcripts	MC											
			MC cord	MC blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo (small)	Eo4 (small)	Ne (small)	Ne3 (small)	Ne4 (small)	pl
207539_s_at	NM_000589.1	IL-4	0.2	0.7	10.4	16.9	134	0.1	0.3	0.0	12	0.2	0.0	0.1
210254_at	L35848.1	R	0.8	0.4	115.6	130.1	153.6	24	17	17	0.1	0.9	3.6	0.5
205513_at	NM_001062.1	vitamin B12 binding protein	15	12	98.9	149.3	110.9	32	22	16.1	19	4.9	4.5	6.3
206148_at	NM_002183.1	IL-3R	1.0	0.7	6.2	80.2	71.3	17	1.8	2.9	0.3	0.4	0.2	0.7
214920_at	R33964	FLJ10226s	0.1	1.1	4.9	13.1	154	0.1	0.2	0.7	0.5	10	0.4	0.5
201825_s_at	AL572542	CGL-49	33	1.6	21.4	74.9	46.5	21	12	0.1	1.2	0.1	0.7	1.7
213238_at	AI478147	ATPase, Class V type 10D	12	2.9	39.9	76.3	118.9	23	1.7	3.1	1.9	2.1	1.4	2.3
211734_s_at	BC005912.1	R	105	28.4	210.0	220.8	262.2	84	2.1	4.8	29	0.3	0.7	45
213694_at	BF447745	Fepsilon RI alpha	0.1	0.1	3.7	13.0	15.6	0.3	0.4	0.4	0.9	0.7	0.7	0.6
206363_at	NM_005360.2	KRA0560	3.7	1.4	36.5	75.7	66.4	12	0.1	0.2	0.2	0.1	0.1	0.5
203373_at	NM_003877.1	c-MAF	2.1	3.9	21.7	85.0	112.2	46	4.7	9.4	6.5	0.7	1.2	0.3
207538_at	NM_0020589.1	SOCS2	0.3	0.1	5.4	9.8	9.2	0.4	0.4	0.0	0.3	0.1	0.0	0.4
213694_s_at	BF671400	IL-4	0.6	0.7	11.1	21.0	20.6	19	1.6	2.4	1.8	0.8	0.6	1.5
209560_s_at	D43958.1	LIM-protein	10.4	2.4	53.2	131.1	90.5	85	7.0	13.8	113	0.5	0.5	42
220234_at	NM_00040562	AML1b protein	0.4	0.1	11.7	10.2	6.0	1.2	0.1	0.2	0.4	0.8	0.9	0.5
210643_at	AF053712.1	carbonic anhydrase VIII	0.1	0.3	1.8	3.4	6.0	0.7	0.4	0.3	0.1	0.1	0.3	0.1
209211_at	AF132081.1	osteoprotegerin ligand	0.1	0.0	1.8	10.2	8.8	0.3	0.5	1.5	0.8	1.1	0.7	0.2
204309_at	NM_000781.1	colon Kupffer-like factor	0.3	0.1	2.6	6.1	5.6	0.1	0.3	0.5	0.5	1.0	0.1	0.3
203372_s_at	AB004903.1	CYP11A	0.6	1.6	9.2	8.5	15.9	14	2.4	0.9	0.2	0.7	0.6	0.4
207463_x_at	NM_002277.1	SOCS2	1.0	1.0	4.8	10.0	10.9	0.4	1.0	1.0	1.2	1.2	0.9	1.8
		serine protease 3 (trypsin 3)												0.4
		acid sphingomyelinase-like												0.6
														0.3
														0.7
														12
														6.7218

Probe set	Accession #	Transcripts	MC												MC											
			cord blood	MC, lung	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Ba 4 (small)	Eo 1 (small)	Eo 2 (small)	Eo 3 (small)	Eo 4 (small)	Ne 1 (small)	Ne 2 (small)	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	CD19	Fb	Ba SL		
213624_at	AA875600	phosphodiesterase	4.7	20	20.8	30.6	25.9	21	28	3.8	1.7	0.5	1.1	1.3	0.1	0.2	0.1	3.8	0.2	3.2	6.6846					
214873_at	AL137651.1	clone DKFZp43400213	0.1	0.4	3.7	15.5	24.4	20	0.9	2.5	2.3	0.2	0.1	0.7	0.6	0.1	1.1	1.5	0.5	0.6	0.7	6.2585				
204928_s_at	NM_019848.2	protein P3	23	15	9.8	49.0	34.3	37	3.3	4.8	42	1.6	1.0	1.9	2.2	4.1	1.8	3.0	0.8	2.0	2.6	6.2142				
208935_s_at	L781321	prostate carcinoma tumor antigen (pcta-1)	22	12	9.9	19.1	16.6	23	1.5	3.6	25	1.1	1.1	1.9	0.9	1.8	1.8	2.0	2.0	1.4	0.8	6.2011				
208201_at	NM_000303.1	phosphomannomutase 2 (PMM2)	1.8	0.3	10.7	15.9	65	0.9	0.6	1.2	0.9	0.8	0.4	1.1	1.3	1.0	1.3	1.2	1.2	1.1	1.7	6.1557				
201826_s_at	NM_01602.1	CG49	1.8	3.1	11.0	27.5	15.1	1.6	1.1	1.4	2.1	1.1	1.4	1.3	1.8	1.6	1.1	1.1	1.1	0.6	2.9	5.6407				
213421_X_at	AW007273	serine protease 4 (trypsin-4)	1.8	1.7	5.9	12.5	11.4	1.0	0.5	1.2	0.5	1.2	1.7	1.2	1.2	0.9	1.0	1.2	1.0	1.0	0.4	1.7	5.4082			
208948_s_at	AF055376.1	c-MAF, short form	6.4	4.9	29.6	47.7	42.3	0.8	0.3	0.4	0.6	0.3	0.0	0.9	1.4	1.0	1.0	1.1	1.1	0.7	0.7	1.4	5.3183			
213342_s_at	AL041124	hypothetical protein PPI665	0.9	0.2	12.2	17.0	12.0	35	1.7	0.5	0.6	0.1	0.3	0.8	0.4	0.6	1.5	2.6	0.7	1.6	1.3	5.2271				
202491_s_at	NM_003640.1	I kappa B-associated protein	1.6	3.8	23.9	51.9	43.5	4.6	4.0	7.1	7.3	1.6	2.1	2.5	2.3	1.7	3.7	7.4	3.2	4.7	4.2	5.107				
221021_s_at	NM_031087.1	Bovine P4 protein	6.9	3.2	7.2	29.2	58.9	28	3.2	5.4	6.3	0.9	1.2	1.8	1.6	1.6	2.2	2.4	2.0	3.5	1.8	4.9129				
213346_at	BE749563	hypothetical protein BC015148	2.7	1.8	17.5	38.8	25.8	40	6.7	6.2	4.8	14	0.9	0.8	1.1	0.2	1.2	1.5	0.6	1.1	1.9	4.8879				
209764_at	AL022312	mannosyl (beta-1,4)-glucoprotein	0.0	0.9	4.1	6.1	5.8	0.8	1.4	0.9	1.4	0.6	0.1	0.5	0.2	1.0	0.4	0.2	0.2	0.4	0.3	4.855				
207067_s_at	NM_002112.1	histidine decarboxylase	64.1	14.7	105.2	164.9	165.7	34	1.4	4.1	28	2.1	1.2	4.6	14.0	24	0.8	0.9	1.1	0.7	0.2	4.6305				
210375_at	X83858.1	GPR	1.0	0.6	2.4	11.5	17.0	0.3	0.1	0.1	0.0	0.4	0.7	0.9	0.7	0.6	0.3	0.2	0.2	0.5	4.6103					
206306_at	NM_001036.1	prostaglandin E receptor, type 3a2	2.1	1.1	3.7	11.0	7.8	1.0	0.6	1.5	0.5	1.2	0.3	1.5	0.9	1.1	0.7	0.3	1.0	0.2	0.4	4.5552				
210001_s_at	AB005043.1	ryanodine receptor 3 (RyR3)	52	0.2	3.0	24.1	29.9	21	3.0	3.2	3.4	0.3	1.0	0.8	1.3	0.8	0.8	0.8	0.8	0.0	0.8	0.9	4.5248			
204614_at	NM_002575.1	SC51	0.3	0.6	5.3	12.9	12.5	0.4	2.4	4.2	2.0	1.0	0.8	0.7	0.3	1.9	0.5	0.7	2.1	0.2	0.2	4.5061				
209860_at	X16323.1	serine (or cysteine) proteinase inhibitor, class B (ovalbumin), member 2 (SERPINB2)	0.4	0.0	2.3	7.3	55	0.5	0.4	0.6	0.5	0.1	0.1	1.0	0.6	0.7	0.1	0.0	1.0	0.0	0.5	4.4335				
209212_s_at	AB030324.1	hepatocyte growth factor (HGF) transcription factor BTEB2	0.1	0.2	7.5	14.3	22.1	23	2.0	4.9	3.7	1.2	1.3	1.5	2.5	1.4	0.5	0.2	1.1	0.9	0.8	4.363				

## A. Basophil (Ba)-selective transcripts (2/2).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba 1	Ba 2 (small)	Ba 3	Ba 4	Ne 1 (small)	Ne 2 (small)	Ne 3 (small)	Ne 4 (small)	CD4	CD8	CD14	CD19	FB	Bas 1			
214651_S_at	U41813_1	Class 1 homeoprotein (HOXA9) DKFZp340B316 si	0.6	1.7	6.3	0.3	0.5	0.1	0.5	1.0	0.1	0.1	0.1	0.1	0.1	0.1	0.1	436118			
32502_S_at	AL04124	catenin (cadherin-associated protein) alpha 2 FLJ2191	1.6	1.9	14.6	2.25	17.4	4.0	2.1	1.4	1.1	0.4	0.4	2.3	2.5	4.1	2.5	43594			
205573_at	NM_004889_1	I kappa B-associated protein FLJ21472	0.2	0.7	1.1	3.9	3.2	0.6	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	42308			
219876_at	NM_025231_1	beta2-chimaerin oncostatin M	0.3	0.7	2.5	7.3	12.0	0.9	0.2	1.9	0.2	1.5	0.7	0.5	1.8	0.2	1.4	42135			
213385_at	AK026415_1	oncostatin M	0.4	0.9	0.9	5.4	4.4	0.2	0.7	0.7	0.7	0.1	0.1	0.1	0.1	0.1	0.4	42131			
214637_at	AF153419_2	catenin (cadherin-associated protein) alpha 2 FLJ2191	0.2	0.2	1.3	3.6	2.2	0.4	0.4	0.5	0.1	0.1	0.1	0.1	0.3	0.2	0.2	41747			
202940_at	NM_024837_1	nemo-like kinase FLJ14135 fs; done MAMMA1002728	4.1	1.4	1.3	6.2	9.1	1.1	0.8	0.6	1.9	0.8	0.6	1.1	0.7	0.6	0.8	0.3	41718		
220416_at	NM_016231_1	AVT66925	0.1	0.1	2.1	3.5	5.1	0.5	0.7	0.8	0.6	0.5	0.1	0.1	0.1	0.1	0.1	0.4	41558		
218118_S_at	AV00891	ET52 intronic transcript 1 mRNA DKFZp340F205	0.6	1.4	31.1	86.8	63.8	3.6	2.2	0.9	0.9	0.1	0.1	0.1	0.5	0.1	0.5	0.1	41491		
221501_at	AL136877_1	MAP kinase activating death domain vets avian erythroblastosis virus E26	0.6	1.4	2.8	50	17.3	31.9	44.5	9.1	83	43.3	1.9	5.7	1.1	0.1	0.1	40555			
222052_S_at	AB002556_1	oncogene homolog 2 FLJ2876	5.6	4.6	12.7	35.0	40.7	6.2	6.1	7.0	8.3	22.1	1.9	2.7	5.4	3.0	3.5	1.1	3.8424		
201328_at	AL575509	histamine H4 receptor chromosome-associated polypeptide C lectin galactoside-binding, soluble, 8 (galectin 8)	1.7	0.7	18.4	34.7	50.7	28	1.6	1.7	1.8	64	9.9	8.7	8.9	0.5	0.1	1.7	3.8075		
218392_X_at	NM_022554	GPR	1.2	1.0	3.5	7.5	7.4	1.4	1.0	1.9	1.2	0.5	1.3	1.9	0.9	1.4	0.5	1.4	3.7324		
205046_at	NM_001813_1	DKFZp340fs; done MAMMA1003026	0.9	0.3	1.5	8.1	13.1	1.7	0.5	1.9	1.1	0.9	1.5	0.9	1.0	0.6	0.6	0.7	3.6719		
221170_at	AF312301	histidine triptorin	0.6	0.8	35.9	34.2	32.5	7.8	11.9	8.7	9.3	0.2	0.8	0.8	0.5	0.6	0.6	0.6	3.6472		
201663_S_at	NM_005096_1	GPR	22	43	17.6	15.1	18.1	3.4	66	4.9	42	4.0	3.7	2.2	2.7	1.7	2.9	1.7	3.6472		
208933_S_at	AI659005	GATA-binding protein 2 fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1)	11.8	4.9	26.7	28.3	28.2	5.9	66	10.1	4.8	3.8	4.5	5.5	2.1	4.3	7.2	4.3	3.6311		
209710_at	AL563460	DKFZp340F205	50.4	38.9	141.1	189.2	154.7	44	13	3.8	3.1	0.7	1.2	5.4	10.8	2.5	0.7	0.3	3.6251		
205769_at	NM_003645_1	KIAA0207	33	25	7.0	16.2	92	0.3	0.3	0.3	0.5	0.1	0.4	0.2	0.3	0.2	0.4	0.1	35389		
209409_at	D8562_1	KIAA0207	8.4	26	12.5	38.0	33.1	4.9	42	12.3	10.4	1.7	1.7	2.1	1.8	1.4	0.7	1.5	3.4907		
38398_at	AB002556	KIAA0358	55.5	41	13.8	24.6	29.8	6.1	6.4	5.6	7.0	3.0	3.2	3.3	4.1	5.1	3.7	4.4	3.4534		
205996_at	NM_003914_1	cyclin A1	55.6	36	16.2	20.6	10.5	0.1	0.6	0.9	0.1	1.6	0.1	0.8	0.4	1.9	0.7	0.3	3.3824		
218195_at	NM_012997_1	DKFZp340F205	8.2	5.3	37.6	56.6	54.6	8.1	8.6	14.0	12.1	3.9	5.0	7.7	9.6	3.8	8.1	1.4	3.3745		
213197_S_at	AI338837	ziculin related factor 1	2.1	1.8	8.4	13.4	16.7	4.8	2.1	4.8	3.7	1.8	1.2	1.2	1.6	0.3	3.3767	3.3342			
208158_S_at	NM_018030_1	oyster-binding protein-related protein	12	23	8.8	18.0	15.3	0.6	0.8	1.6	1.4	1.5	2.3	2.7	1.8	2.0	0.2	1.3	0.5	4.0	
210109_at	AF191492_1	nasopharyngeal carcinoma associated gene protein 8	12	0.7	3.6	6.4	4.2	1.2	1.6	1.0	0.3	0.6	1.1	1.7	0.6	0.2	1.3	0.5	0.1	3.2977	
220918_at	NM_021431_1	FLJ28556	10	1.1	26.1	37.3	26.2	6.2	6.5	14.1	11.3	3.3	2.5	2.0	2.0	1.1	0.9	0.9	3.2902		
208159_X_at	C345986_1	am 1 (acute myeloid leukemia, very oncogene)	12	0.1	3.1	7.2	7.1	2.5	1.6	1.6	1.1	0.2	1.0	0.6	1.4	0.7	1.0	0.8	0.1	3.2789	
212412_at	NM_03041_1	exonuclease NFE-sp	3.6	7.6	7.8	30.6	20.1	1.6	2.3	2.7	0.8	0.6	0.2	1.5	1.0	0.2	0.3	0.2	0.1	3.2336	
210109_at	AV715767	chromosome 16 BAC clone	182	162	41.3	72.5	67.3	7.7	7.7	16.3	11.6	6.4	6.3	9.1	12.7	3.7	3.1	4.1	8.0	3.2017	
215715_S_at	AC004581	CTBP275K-4M2	2.9	2.5	4.8	12.8	104	0.6	0.9	1.4	0.8	0.1	0.0	0.2	0.8	0.1	0.4	0.3	3.198		
221509_at	AB014731_1	SMAD-3	7.6	5.4	13.2	48.5	32.4	5.2	5.7	18.1	10.7	3.5	3.8	11.4	8.1	2.8	5.6	6.0	3.1618		
218837_at	NM_018439_1	hypothetical protein IMPACT	1.3	2.4	2.9	10.7	9.3	1.5	1.5	1.7	2.1	0.6	0.7	0.6	0.6	1.2	0.9	1.1	2.1	3.1587	
218552_at	NM_018191_1	hypothetical protein FLJ10716	0.8	0.5	4.9	13.7	8.7	2.3	1.7	3.4	3.9	1.0	2.0	2.8	3.6	0.8	2.3	2.0	1.7	3.1038	
213035_at	A1081194	KIAA0379	2.1	3.8	11.1	26.7	22.4	2.5	1.5	3.4	25	1.9	1.1	2.3	1.6	4.6	2.5	1.3	0.1	3.0937	
21180_X_at	D89788_1	lactoferrin	1.5	0.2	3.1	9.4	7.5	2.0	2.5	1.7	1.0	1.4	0.3	1.7	0.4	0.6	0.4	0.7	0.2		
210731_S_at	AL136105	lactoferrin	2.1	1.7	4.8	9.1	6.4	1.9	1.8	3.0	1.8	1.2	1.4	2.7	1.4	2.2	1.2	1.7	3.0876		
203164_at	BE464756	acetyl-Coenzyme A transporter	2.3	1.9	3.7	12.6	12.4	2.5	1.9	1.9	2.7	1.1	0.6	1.2	1.7	2.3	2.6	2.1	2.7	3.063	
205768_S_at	NM_003645_1	lactoferrin	3.0	1.7	3.9	10.7	7.7	0.4	0.1	0.6	0.2	0.1	0.8	0.1	0.7	0.0	0.8	0.1	0.1	3.0353	
210517_S_at	AB003476_1	lactoferrin	25.1	4.9	44.0	69.5	59.6	1.5	0.4	0.6	0.8	0.1	0.2	1.0	3.0	0.9	0.8	0.1	0.3	3.0146	
210647_X_at	AF102988_1	lactoferrin	2.3	1.1	18.7	13.2	9.1	3.4	3.3	4.0	4.5	3.3	5.0	4.2	3.6	1.8	3.5	4.4	1.8	2.2	3.002

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## SUBSTITUTE SHEET (RULE 26)

Fig. 6B

## B. Eosinophil (Eo)-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC cond blood	MC lung	Ba1 (small)	Ba2 (small)	Eo	Eo3 (small)	Eo4 (small)	Ne 1 (small)	Ne 2 (small)	Ne 3 (small)	Ne 4 (small)	CD4	CD8	CD14	CD19	FB	EoSL			
207378_at	NM_0014011	15-lipoxygenase	0.1	0.6	0.7	0.7	145	246	183	17.0	0.1	1.1	0.1	0.1	0.0	0.1	0.0	74.129				
219695_at	NM_047031	FLJ22593	0.0	1.0	1.8	1.1	298	347	248	27.8	0.8	1.5	0.4	0.9	0.1	0.6	0.4	0.1	19.123			
208253_at	NM_0144421	R	0.0	2.4	0.4	0.4	17.1	23.1	17.6	11.8	0.7	0.4	0.1	0.8	0.3	0.2	0.5	0.2	9.8056			
211922_s_at	AY0285321	stcatalase	3.7	2.2	6.2	6.8	22	782	1345	1197	88.8	162	13.0	8.8	8.7	2.2	2.9	11.1	75	4.6	9.125	
201802_at	NM_0049551	solute carrier family 29 (nucleoside transporters)	4.8	2.8	2.9	3.4	19	248	304	36.1	423	0.1	0.6	0.6	0.8	0.2	0.9	0.3	2.2	1.0	1.1	8.989
214533_at	NM_0018051	CCAAT enhancer binding protein (CEBP) epsilon	0.1	0.1	0.7	1.2	12	7.9	11.4	23.4	17.3	1.8	1.5	1.9	1.1	1.4	0.5	0.4	1.0	0.1	0.1	8.9462
210029_at	N344551	interleukin-gamma-inducible indolectamine 23-dioxogenase	0.7	0.1	5.3	42	26	200	390	33.4	295	1.6	2.1	23	1.8	1.7	1.5	1.7	0.3	1.4	0.9	7.7078
215573_at	AU147084	SLC12A7	0.1	0.1	0.5	0.3	1.1	9.8	84	16.9	72	0.4	1.9	1.8	20	0.1	0.1	0.1	0.4	0.0	7.5983	
201801_s_at	AF0791171	SLC12A7	3.5	1.9	1.7	0.5	0.9	297	47.1	7.4	11.0	0.1	0.5	0.4	0.7	1.1	0.4	0.1	1.4	0.6	1.0	7.3114
213825_at	AF2215201	oligodendrocyte lineage transcription factor 2	0.4	0.6	0.2	0.4	0.6	6.0	10.9	18.7	12.5	0.8	0.9	1.5	1.0	0.6	1.7	0.3	0.4	0.3	0.3	6.5987
219821_s_at	NM_0189881	glucose-fructose oxidoreductase domain containing	3.0	1.4	1.8	2.6	23	187	173	30.9	31.3	3.9	3.1	24	2.9	3.2	1.3	2.5	3.0	3.8	0.8	6.2284
205472_s_at	NM_0043921	dachshunk (Drosophila) homolog	0.0	0.1	0.1	0.4	0.1	27	14	2.2	1.7	0.3	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.1	0.0	6.0088
202188_at	NM_0146691	KIAA0095	0.5	0.9	0.4	1.8	12	6.8	85	135	10.6	0.2	0.2	0.2	0.1	0.2	0.3	1.7	1.7	1.4	0.4	5.4499
210548_at	U589713	chemokine CCL23	0.6	1.3	0.4	1.7	0.5	55	62	42	6.9	0.1	0.9	0.7	0.2	0.3	0.1	0.2	0.6	0.1	0.1	5.3082
209447_at	AF0433901	lymphocyte membrane associated protein (LAMP)	0.6	0.5	2.5	34	36	41.8	497	66.2	60.1	0.2	0.9	0.5	12	2.6	5.1	10.4	1.6	6.3	2.7	5.1472
206171_at	NM_0006772	ADORA3 adenosine A3 receptor	2.3	2.3	2.8	37	22	7.8	13.9	22.0	17.9	1.6	3.1	2.2	2.5	1.2	1.6	0.5	2.0	0.5	0.5	5.0469
210549_s_at	U589131	chemokine CCL23	1.1	1.1	0.1	1.3	0.6	7.9	5.6	27	8.1	0.0	0.6	0.0	0.2	0.1	0.1	0.1	0.2	0.0	0.4	4.9873
214183_s_at	X918171	transketolase-like protein	0.1	0.2	0.2	0.7	0.1	32	40	6.6	7.2	0.2	0.2	0.7	0.1	0.2	0.2	0.1	0.1	0.6	0.0	4.7894
215550_at	AB0330881	specinin repeat containing, nuclear envelope	0.1	0.1	0.5	0.1	0.1	3.8	42	3.0	28	0.0	0.1	0.2	0.4	0.7	0.2	0.1	0.0	0.1	0.2	4.7822
206277_at	NM_00225641	GPR	0.1	0.1	0.1	0.2	0.1	34	4.7	8.1	5.9	0.1	0.3	0.1	0.1	0.2	0.1	0.3	1.2	0.2	0.1	4.5043
204776_at	NM_0032481	thrombospondin 4 (THBS4)	0.8	0.7	1.5	0.1	0.8	32	59	10.0	6.4	1.8	1.4	0.6	0.9	0.3	0.2	0.3	1.4	1.1	1.2	4.1746
201332_at	L296081	L-iditol 2,4-dihydroxylase	4.1	2.6	3.5	11.4	128	22.5	29.9	49.0	37.0	18	3.0	4.4	2.2	2.1	1.6	1.2	2.7	2.5	1.8	4.1557
206637_at	NM_0148791	P2YX purinergic receptor GPR105 for UDP-glucose	5.7	1.6	13.3	19.9	135	44.2	55.1	81.4	62.4	18	9.3	15.4	9.2	0.7	0.9	0.8	0.0	5.5	0.1	3.8761
213622_at	A1733465	collagen type IX, alpha 2	1.5	1.4	1.9	1.2	1.3	10.3	9.6	6.6	8.8	2.7	2.1	2.1	2.2	0.7	1.2	1.2	2.2	1.7	0.9	3.6576
214705_at	A0013061	PDZ domain protein	0.1	0.1	0.4	0.3	0.1	21	15	26	22	0.3	0.0	0.6	0.7	0.1	0.4	0.3	0.3	0.6	0.1	3.6532
213930_at	L33930	CD24 signal transducer	0.2	0.7	3.0	0.3	0.8	11.9	14.0	18.8	13.9	0.1	0.1	0.3	0.8	0.9	0.0	0.1	4.3	0.2	3.3793	
201432_at	NM_0017521	catalase (CAT)	23.0	14.3	35.7	49.4	199	2023	209.7	221.6	207.3	67.0	54.3	71.3	60.9	92	11.2	15.1	53.6	29.9	21.4	3.3325
209696_at	D260541	fructose-1,6-bisphosphatase	0.9	3.4	43	11.1	64	202	227	28.8	32.5	3.0	2.5	2.4	10.9	2.0	15	8.1	1.1	0.6	3.3089	
216379_at	AK0001681	CD24 signal transducer	1.3	1.4	16.2	0.9	15	66.1	70.1	81.9	77.9	1.7	2.8	2.6	4.1	4.8	0.5	0.6	0.9	2.5	0.5	3.2741
205569_at	NM_0149981	lysosome-associated membrane protein	0.4	0.2	0.7	0.1	0.4	24	3.1	6.8	3.0	0.6	0.1	1.4	0.8	0.4	1.1	0.7	0.1	0.1	0.5	3.2308
219233_s_at	NM_0185301	gastrointestinal tumor-associated antigen GATA3-1	0.1	1.9	2.1	4.6	54	75	85	21.8	21.2	0.8	0.1	1.5	2.1	0.1	1.1	0.1	0.1	0.1	0.5	3.2093
202286_s_at	J04152	semenogelin I (SEMG1)	0.9	0.7	1.3	0.3	0.1	1.1	2.5	8.7	1.8	0.4	0.8	0.6	0.6	0.2	0.7	0.3	0.5	0.1	3.1844	
206442_at	NM_0030071	Bloom syndrome	0.6	0.7	0.4	0.0	0.1	12	3.2	4.9	3.4	0.3	0.2	1.1	1.9	0.1	0.2	0.2	0.9	0.4	0.1	3.1837
205733_at	NM_0005571	calcium/calmodulin-dependent protein kinase (CaMK)	1.9	1.1	2.0	24	22	85	6.0	7.5	11.2	2.1	2.0	1.0	1.2	12	2.4	1.8	1.7	2.6	1.2	3.1427
204892_at	NM_0036562	DKFZp586C619	4.0	1.1	6.3	8.9	64	17.8	19.3	24.9	26.5	0.6	0.2	1.8	1.5	0.1	1.4	1.0	3.0	0.6	1.8	3.0763
213497_at	AL0503741	similar to ankyrin repeat-containing protein AKR1	1.0	0.7	1.0	1.3	1.6	6.3	68	6.0	23	3.0	1.4	2.3	2.0	0.4	0.5	1.6	1.7	0.8	3.0099	
219296_at	NM_0190281		22	1.7	2.0	3.5	1.6	7.3	4.4	8.4	7.4	1.8	2.4	2.4	2.3	0.1	1.4	1.6	1.3	1.9	0.8	3.0018

### C. Neutrophil (Ne)-selective transcripts (1/7).

## **SUBSTITUTE SHEET (RULE 26)**

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## C. Neutrophil (Ne)-selective transcripts (2/7).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	MC Ba1 (small)	MC Ba2 (small)	MC Ba3 (small)	MC Ba4 (small)	MC Eo1 (small)	MC Eo2 (small)	MC Eo3 (small)	MC Eo4 (small)	MC Ne1 (small)	MC Ne2 (small)	MC Ne3 (small)	MC Ne4 (small)	CD4 pl	CD8 pl	CD14 pl	CD19 pl	CD20 pl	CD45 pl	Ne51					
210789_x_at	LG06522_1	GPR carinoembryonic antigen (CEA)	1.1 0.1	0.4 0.2	1.9 0.4	1.4 0.7	1.5 0.7	1.5 0.3	2.5 0.8	0.4 0.7	194 514	186 677	226 448	155 464	0.7 0.5	0.5 0.5	5.6 5.6	0.7 0.7	0.7 0.4	0.7 0.4	0.7 0.4	0.7 0.4	0.7 0.4	92749 92661				
210772_at	M88107_1	GPR formyl peptide receptor 2	0.7 0.7	0.5 0.2	1.6 1.2	0.2 0.7	0.5 0.6	1.1 0.8	0.9 0.9	0.7 0.7	0.9 0.8	0.5 0.5	0.5 0.5	0.5 0.5	0.5 0.5	0.5 0.5	0.5 0.5	0.5 0.5	0.5 0.5	0.5 0.5	0.5 0.5	0.5 0.5	0.5 0.5	91536				
218978_5_at	NM_015861	Fc gamma R III (CD16)	0.7 0.7	0.2 0.2	1.2 1.2	0.7 0.7	0.6 0.6	0.7 0.7	0.5 0.7	0.5 0.7	0.5 0.7	0.5 0.7	0.5 0.7	0.5 0.7	0.5 0.7	0.5 0.7	90769											
204062_at	NM_005570_1	fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1)	4.3 1.1	2.6 0.8	5.1 3.2	11.5 4.0	19.4 29	5.1 2.8	5.1 4.7	0.8 0.7	0.2 0.2	2.0 2.7	1.4 1.7	1.1 1.2	1.1 1.7	1.1 1.7	1.1 1.7	1.1 1.7	1.1 1.7	1.1 1.7	1.1 1.7	1.1 1.7	1.1 1.7	1.1 1.7	9.8855			
207275_s_at	NM_001995_1	male germ cell-associated kinase nuclear receptor binding factor-2 KCND inward-rectifying potassium channel Kir2.1	0.1 0.1	0.0 0.0	1.3 3.2	0.7 4.0	0.8 2.8	0.7 2.8	0.5 4.7	0.5 0.7	0.2 0.2	2.3 2.7	1.7 1.9	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	8.866			
220302_at	NM_005962	ubiquitin-conjugating enzyme E2D1	0.1 0.0	0.0 0.0	0.9 0.9	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	8.3788														
221803_5_at	AA883074	ICN	1.0 0.0	0.4 0.1	2.5 0.9	4.4 2.0	24 16	4.7 0.6	6.1 1.0	0.5 0.1	0.2 0.1	2.3 2.7	1.7 1.9	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	8.3788			
206765_at	AF153820_1	KCNJ inward-rectifying potassium channel Kir2.1	0.0 0.1	0.1 0.1	0.9 0.9	2.0 2.0	1.6 1.6	0.8 0.8	0.6 0.6	0.5 0.5	1.0 1.0	0.5 0.5	0.4 0.4	0.3 0.3	1.0 1.0	0.4 0.4	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	8.108			
213351_5_at	AI93469	K4A0779	0.0 0.1	0.1 0.1	0.9 0.9	2.0 2.0	1.6 1.6	0.8 0.8	0.6 0.6	0.5 0.5	1.0 1.0	0.5 0.5	0.4 0.4	0.3 0.3	1.0 1.0	0.4 0.4	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	7.8712			
214590_5_at	AI545760	leukotriene B4 omega-hydroxylase (CYP4F5)	0.1 0.1	0.5 0.2	1.3 1.3	6.1 6.1	5.0 5.0	0.2 0.1	0.1 0.1	0.5 0.5	2.8 4.2	7.0 7.9	5.6 5.6	42.8 42.8	30.5 30.5	0.3 0.2	0.1 0.1	7.2 7.2	2.3 2.3	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	7.5773			
206522_at	NM_004668_1	Fc gamma receptor IIc2 VWA3 protein	0.0 0.1	0.0 0.1	0.8 0.2	1.8 1.7	3.3 2.7	8.1 7.1	16.1 16.1	0.1 0.1	0.1 0.1	1.7 1.6	9.6 14.3	7.3 20.3	10.5 14.3	89.0 22.1	52.9 20.0	5.6 3.0	0.6 0.6	0.6 0.6	0.6 0.6	0.6 0.6	0.6 0.6	0.6 0.6	7.5239			
210992_x_at	U909391	R	0.1 0.1	0.0 0.1	1.7 1.3	4.8 4.8	6.5 6.5	4.4 4.4	6.8 6.8	0.1 0.1	0.1 0.1	1.6 1.6	1.1 1.1	1.4 1.4	1.4 1.4	2.5 2.5	4.9 4.9	7.0 7.0	10.7 10.7	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	7.5056			
220528_at	NM_013999_1	early development regulator 2	0.1 0.1	0.0 0.1	1.5 1.5	7.0 7.0	1.5 1.5	1.0 1.0	1.5 1.5	0.6 0.6	0.9 0.9	0.9 0.9	0.9 0.9	0.9 0.9	0.9 0.9	0.9 0.9	0.9 0.9	0.9 0.9	0.9 0.9	0.9 0.9	0.9 0.9	0.9 0.9	0.9 0.9	7.4603				
200919_at	NM_004427_1	glyceraldehyde-3-phosphate dehydrogenase	0.1 0.1	0.0 0.1	1.7 1.7	0.2 0.2	0.8 0.8	0.4 0.4	0.7 0.7	0.7 0.7	0.7 0.7	0.7 0.7	0.7 0.7	0.7 0.7	0.7 0.7	0.7 0.7	0.7 0.7	7.4139										
207387_5_at	X51757	glutamyl-peptide cyclotransferase	0.1 0.1	0.0 0.1	0.9 0.9	0.4 0.4	0.6 0.6	0.6 0.6	0.9 0.9	0.7 0.7	0.7 0.7	0.4 0.4	0.3 0.3	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	7.3246		
205747_5_at	NM_0124132	triggering receptor expression on myeloid cells 1	0.1 0.1	0.0 0.1	1.3 1.3	0.4 0.4	0.2 0.2	0.5 0.5	2.9 2.9	0.7 0.7	1.4 1.4	1.5 1.5	92.8 84.0	84.0 13.0	8.2 13.4	34.0 43	34.0 43	0.6 0.6	0.6 0.6	0.6 0.6	0.6 0.6	0.6 0.6	0.6 0.6	0.6 0.6	0.6 0.6	7.2368		
219434_at	NM_018643_1	thrombomodulin	0.1 0.1	0.0 0.1	1.7 1.7	0.4 0.4	0.2 0.2	0.4 0.4	1.2 1.2	0.1 0.1	0.1 0.1	1.7 1.7	1.6 1.6	1.6 1.6	1.6 1.6	1.6 1.6	1.6 1.6	0.4 0.4	0.4 0.4	0.4 0.4	0.4 0.4	0.4 0.4	0.4 0.4	0.4 0.4	7.1328			
203887_5_at	NM_00361_1	orosomucoid 1 (ORM1)	0.5 0.5	0.1 0.1	0.1 0.1	0.4 0.4	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	7.0823												
205040_at	NM_000607_1	phosphotyrosine kinase	0.2 0.2	0.4 0.4	0.1 0.1	1.2 1.2	1.7 1.7	0.8 0.8	1.1 1.1	0.6 0.6	0.6 0.6	0.6 0.6	0.6 0.6	0.6 0.6	0.6 0.6	0.6 0.6	0.6 0.6	6.966										
214681_at	AI83490	FLJ20723	0.2 0.2	0.4 0.4	0.1 0.1	1.2 1.2	1.7 1.7	0.8 0.8	0.7 0.7	0.4 0.4	0.4 0.4	1.3 1.3	1.7 1.7	47.2 54.4	54.4 91.9	94.0 91.9	1.7 1.7	0.7 0.7	0.4 0.4	0.9 0.9	0.3 0.3	0.3 0.3	0.3 0.3	0.3 0.3	6.9074			
218035_5_at	NM_019277_1	GTPase regulator associated with the focal adhesion kinase pp125(FAK)	1.2 1.2	1.4 1.4	3.5 3.5	5.9 5.9	5.1 5.1	6.5 6.5	5.1 5.1	8.5 8.5	7.1 7.1	43.7 40.6	40.6 45.2	56.0 56.0	0.7 0.7	1.3 1.3	2.9 2.9	5.1 5.1	0.8 0.8	1.2 1.2	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	6.8934		
205068_5_at	BE671084	secretory leukocyte protease inhibitor/leukocyte protease inhibitor (antileukoprotease) (SLPI)	1.7 1.7	0.8 0.8	4.6 4.6	1.5 1.5	1.1 1.1	1.2 1.2	2.2 2.2	0.8 0.8	0.8 0.8	0.8 0.8	162 162	198 198	13.9 13.9	8.7 8.7	18.6 18.6	5.8 5.8	0.5 0.5	0.2 0.2	0.2 0.2	0.8 0.8	0.3 0.3	0.1 0.1	0.1 0.1	0.1 0.1	6.7497	
203021_at	NM_003064_1	chromosome 7 carcinoembryonic antigen subdomains A and B	0.6 0.3	0.4 0.1	0.2 0.1	0.4 0.1	0.1 0.1	0.1 0.1	0.3 0.3	0.7 0.4	0.7 0.4	0.7 0.4	0.3 0.3	28 72	33 91	7.0 7.0	12.1 12.1	0.9 0.9	0.1 0.1	1.9 1.9	10 10	0.3 0.3	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	6.9855	
216316_x_at	X78713	FLJ21458	putative lymphocyte G0/G1 switch gene (G0S2)	0.8 0.8	0.8 1.3	1.9 1.3	0.9 0.7	0.5 0.5	1.1 1.1	0.6 0.6	0.5 0.5	0.5 0.5	0.5 0.5	8.7 18.7	10.1 10	118.0 226.5	52.0 25.0	39.6 11.3	92.5 83.1	1.7 1.2	0.8 0.8	0.1 0.1	0.6 0.6	0.2 0.2	0.34 0.34			
217209_at	X16454	NM_024850_1	transducin-like enhancer of split 3	0.7 0.7	0.7 0.7	1.5 1.3	0.5 0.5	1.3 1.3	2.3 2.1	1.1 1.8	1.0 1.5	0.7 0.7	0.7 0.7	0.7 0.7	19.1 19.1	19.1 19.1	15.9 12.8	13.7 24.8	9.1 12.8	1.1 1.1	1.1 1.1	0.9 0.9	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	6.64779	
220421_at	NM_024850_1	KIAA1547	KIAA0329	0.7 0.7	0.7 0.7	1.5 1.3	0.5 0.5	1.3 1.3	2.3 2.1	1.1 1.8	1.0 1.5	0.7 0.7	0.7 0.7	0.7 0.7	19.1 19.1	19.1 19.1	15.9 12.8	13.7 24.8	9.1 12.8	1.1 1.1	1.1 1.1	0.9 0.9	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	6.64779	
213324_s_at	NM_015714_1	granulocyte colony-stimulating factor receptor	0.1 0.1	0.0 0.0	1.0 1.0	0.1 0.1	0.2 0.2	0.3 0.3	0.6 0.6	0.1 0.1	0.2 0.2	0.2 0.2	0.2 0.2	24 24	220.3 205	187.2 446	134.9 35.8	112.1 42.2	0.2 0.5	0.8 0.8	0.2 0.2	0.2 0.2	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	6.2051	
205472_s_at	NM_005078_1	immunoglobulin superfamily member WM78	0.1 0.1	0.0 0.0	1.0 1.0	0.1 0.1	0.2 0.2	0.3 0.3	0.6 0.6	0.1 0.1	0.2 0.2	0.2 0.2	0.2 0.2	24 24	104.3 146	129.0 35.8	13.7 21.8	14.1 15.5	1.4 1.5	0.9 0.9	0.7 0.7	0.7 0.7	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	6.172	
212769_at	A157426	FLJ11151	Fc gamma receptor IIa (CD32)	0.1 0.1	0.0 0.0	1.2 1.2	0.9 0.9	1.2 1.2	1.8 1.8	1.1 1.3	0.9 0.9	0.9 0.9	0.9 0.9	0.9 0.9	12.0 12.0	12.0 12.0	17.9 15.5	12.8 12.8	14.1 14.1	1.4 1.4	0.9 0.9	0.7 0.7	0.7 0.7	0.1 0.1	0.1 0.1	0.1 0.1	0.1 0.1	6.112
203037_at	AB00295_1	superoxide dismutase 2	0.1 0.1	0.0 0.0	1.2 1.2	0.9 0.9	1.2 1.2	1.8 1.8	1.1 1.3	0.9 0.9	0.9 0.9	0.9 0.9	0.9 0.9															

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## C. Neutrophil (Ne)-selective transcripts (3/7).

Probe set	Accession #	Transcripts	MC <sub>cord</sub> blood	MC <sub>lung</sub>	MC <sub>Ba 1 (small)</sub>	MC <sub>Ba 2 (small)</sub>	MC <sub>Ba 3 (small)</sub>	MC <sub>Eo 1 (small)</sub>	MC <sub>Eo 2 (small)</sub>	MC <sub>Eo 3 (small)</sub>	MC <sub>Eo 4 (small)</sub>	MC <sub>Ne 1 (small)</sub>	MC <sub>Ne 2 (small)</sub>	MC <sub>Ne 3 (small)</sub>	MC <sub>Ne 4 (small)</sub>	MC <sub>pl</sub>	MC <sub>CD4</sub>	MC <sub>CD8</sub>	MC <sub>CD14</sub>	MC <sub>CD19</sub>	MC <sub>Fb</sub>	MC <sub>NeSL</sub>			
207645_at	NM_0013281	retinitis pigmentosa GTPase regulator (RPGR)	0.0	0.6	1.1	2.0	1.2	1.1	1.2	2.1	2.8	7.1	7.0	13.6	15.1	0.2	1.2	0.4	0.9	0.7	0.3	60348			
209850_s_at	BC055496.1	Cdc22 effector protein 2	0.2	0.2	1.3	0.2	0.4	0.5	1.4	1.2	1.2	1.32	0.96	6.67	8.7	0.2	0.2	0.6	0.4	1.6	1.6	53313			
209396_s_at	NM_004994.1	matrix metalloproteinase 9	47.7	0.6	1.6	1.9	1.4	1.2	2.4	1.55	1.5	365	351	368	219	17	20	1.4	1.9	1.3	1.4	53311			
215966_X_at	AK292874	glycerokinase	12	0.2	0.6	0.1	1.2	0.2	1.0	1.2	1.2	66	102	73	74	0.2	0.1	0.2	1.3	0.5	0.0	53077			
206925_at	NM_005668.1	stearoyltransferase 8	3.1	1.2	2.1	2.5	2.0	1.4	3.1	1.6	1.6	21.7	33.3	6.8	11.4	0.4	0.9	1.6	2.6	1.2	0.2	50688			
2117645_at	BC005980.1	ubiquitin-conjugating enzyme E1	1.8	1.4	2.1	2.9	2.4	2.5	5.7	3.9	2.2	29.3	31.2	52.6	25.4	0.2	2.0	1.4	5.7	1.3	2.3	53143			
2011925_at	NM_006324.1	phosphotidylinositol transfer protein (PTPN)	3.0	3.1	1.9	5.0	4.6	3.9	5.4	6.6	5.4	27.9	26.9	32.9	35.2	2.0	3.5	3.7	5.0	3.2	2.8	5811			
2059215_at	UT6120.1	placental taurine transporter	1.2	0.7	0.5	0.2	0.4	0.3	1.6	0.5	0.9	14.8	17.2	2.8	2.6	0.0	0.7	0.3	1.1	0.3	0.4	53909			
2091375_at	BC000263.1	omega-quinolinic acid-terminal hydrolase related polypeptide	3.6	4.1	2.0	2.6	1.9	1.5	0.9	2.7	0.9	25.0	24.5	37.6	29.7	3.5	5.0	2.5	3.5	2.7	3.0	53864			
2080525_at	NM_001815.1	calcineurin/beta antigen-related cell adhesion molecule 3 (CEACAM3)	1.7	1.4	2.9	2.7	1.9	3.0	2.6	2.8	2.1	14.3	16.5	20.0	13.7	2.5	1.3	2.3	2.8	2.5	1.6	53572			
2198735_at	NM_008176.1	insulin-like growth factor 2 receptor	6.4	2.8	0.2	0.8	1.8	4.1	5.4	6.8	5.4	82.4	106.9	80.1	71.7	1.7	29	8.7	84	48	14.8	53104			
2198145_at	NM_019169.1	ELU10622	1.2	1.0	6.9	13.7	12.5	3.2	3.3	7.7	5.8	52.7	54.4	82.8	88.3	29	87	11.8	32	10.8	1.3	53642			
2020845_at	NM_00303.1	SEC14 (S, cerevisiae)-like 1	5.7	2.5	12.8	28.8	22.6	20.6	18.7	35.5	29.5	131.7	129.7	155.6	179	192	4.1	35	11.5	77	11.8	1.5	53423		
32069_at	AB074515	KIAA0615	28	15	2.1	5.6	5.5	4.6	3.7	5.9	6.9	23.9	20.9	35.1	40.5	1.0	3.4	3.3	26	2.1	1.5	53348			
205896_at	NM_003059.1	solute carrier family 22 member 4 (SLC22A4)	0.8	1.2	1.0	0.7	1.1	1.9	2.4	3.5	2.7	8.5	13.3	30.0	12.6	0.5	0.7	0.8	2.6	1.5	1.4	54612			
205584_at	NM_015164.1	MD-2 protein	7.4	1.1	2.0	3.9	1.8	1.0	0.4	0.6	0.5	43.9	62.3	87.8	560	1.3	0.7	0.8	1.1	0.5	0.4	54459			
2020825_at	NM_003003.1	SEC14 (S, cerevisiae)-like 1	10	0.3	3.6	2.5	2.2	15.5	5.4	12.3	8.4	40.2	57.3	54.9	60.9	3.8	0.8	1.3	2.7	3.3	2.4	54422			
2043038_at	NM_014844.1	KIAA0329	2.9	1.1	2.2	2.8	2.8	2.1	3.1	3.1	3.1	43	16.5	19.9	19.0	3.4	1.3	1.7	1.8	1.3	2.5	53369			
2075005_at	NM_004547.1	caspase 5	0.3	1.1	0.1	0.0	0.1	0.7	0.3	0.2	0.5	42	6.2	4.6	2.9	0.3	0.4	0.8	0.1	0.3	0.3	53379			
2034355_at	NM_007787.7	CD10 membrane metallo-endopeptidase	0.3	0.5	0.4	0.3	0.2	0.1	0.3	0.3	0.2	16.4	44.2	54.6	42.8	0.2	0.3	0.2	0.2	0.2	0.9	52591			
205539_at	NM_006576.1	advillin	0.4	0.5	2.0	1.4	0.8	1.0	1.1	1.0	1.1	84	69	60	10.1	1.0	1.3	0.4	1.5	0.7	1.1	52441			
204601_at	NM_014664.1	KIAA0615	1.9	1.2	1.3	3.2	2.3	3.0	2.7	3.7	3.0	12.9	12.8	20.2	20.0	0.1	2.2	2.6	1.3	1.9	1.0	52381			
201963_at	NM_021122.2	faty-acid-Coenzyme A ligase, long-chain 1 (FATCL1)	29	21	5.0	19.9	33.4	6.6	3.8	10.3	6.1	58.8	86.6	92.2	80.2	0.1	1.1	1.1	1.1	1.0	1.5	23374			
2070645_at	NM_009590.1	GPR	0.7	0.1	0.9	0.9	0.8	0.8	0.8	0.9	1.2	43	4.7	4.0	6.6	0.8	0.5	0.8	0.5	0.8	0.3	51905			
2200005_at	NM_023914.1	P2YX purinergic receptor GPR86 for UDP-glucose	0.6	0.0	0.1	0.1	0.1	19.7	9.6	25.1	173	765	771	100.7	98.6	1.9	0.1	0.2	12.3	0.6	0.0	51686			
211395_at	U95340.1	R	46	0.3	7.3	9.7	15.1	19.5	44	6.6	15.0	14.0	3	42.9	38.9	3.0	14	0.6	14.0	7.2	10	51401			
2017805_at	AB04518.1	GSK-3 binding protein FRAT2	4.4	2.8	3.5	9.2	80	13.4	16.9	27.3	22.6	93.2	97.2	100.6	104.2	13	19	2.9	10.2	2.5	10	51305			
209845_at	U813793	ring finger protein 13 (RNF13)	3.4	2.9	5.9	17.5	33.5	17.7	11.7	12.6	15.1	64.9	88.3	73.0	80.2	24	63	29	13.8	12.6	1.1	50403			
218319_at	NM_006512	phorbol	0.6	1.1	1.0	1.2	2.6	1.3	0.8	3.9	0.5	19.6	11.1	30.8	0.5	15	0.2	0.4	1.0	1.2	50277				
2066325_at	NM_004900.1	BK7456133	11.7	6.2	4.6	18.5	12.5	5.0	3.3	8.2	4.9	11.5	11.7	12.5	12.5	2.6	5.3	4.2	4.1	4.4	4.3	49958			
2208905_at	NM_005938.1	apolipoprotein 1	0.7	2.8	0.6	2.1	1.6	2.0	0.4	1.8	1.1	8.0	3.9	12.7	52	0.2	0.9	0.4	1.4	1.7	0.4	49332			
2216535_at	BC004395.1	CO2 prostaglandin-endoperoxide Synthase 2	6.5	16.2	0.6	24	1.6	1.3	2.2	15	20	850	78.5	75.2	52.9	1.9	0.4	0.6	44.6	91.8	0.4	43	0.3	0.5	49206
204748_at	NM_00963.1	integral membrane protein PAR2 protease activated receptor-2	0.8	0.8	0.9	0.2	0.9	1.1	0.2	0.8	1.1	0.1	1.5	4.1	4.1	1.3	1.5	0.2	1.5	0.3	0.7	48845			
2104235_at	L321785.1	GPR	0.6	0.9	1.2	1.5	1.2	1.2	1.5	1.5	2.2	8.4	6.0	87	7.7	1.6	0.9	1.5	1.0	1.0	1.3	48508			
206459_at	AB034469	KIAA079	0.1	0.6	0.3	0.2	0.0	1.7	2.7	2.0	8.6	19.0	15.0	13.9	0.4	0.3	2.9	1.3	1.3	1.3	48373				
2133325_at	U813793	interleukin-13 receptor	2018885_at	U813793	R	0.1	0.6	0.3	0.2	0.0	1.7	2.7	2.0	8.6	19.0	15.0	13.9	0.4	0.3	2.9	1.3	1.3	1.3	4746	

### C. Neutrophil (Ne)-selective transcripts (4/7):

Probe set	Accession #	R	Transcripts	MC <sub>cord</sub>	MC <sub>lung</sub>	Ba <sub>1</sub>	Ba <sub>2</sub>	Ba <sub>3</sub>	Eo	Eo	Eo <sub>3</sub>	Eo <sub>4</sub>	Ne	Ne <sub>2</sub>	Ne <sub>3</sub>	Ne <sub>4</sub>	Fb	Ba <sub>5</sub>		
2029470_s_at	AA164731	R	CD95,Fas,APO-1	1.4	1.4	1.4	1.4	1.4	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5		
2029310_s_at	U258041		lch-2 cysteine protease phosphatidylinositol glycan, class B (PGB)	2.5	1.9	2.1	1.7	1.9	1.4	1.3	1.3	1.4	1.9	1.3	1.3	1.3	1.3	1.3	1.3	
205452_s_at	NM_0048551		FLJ20950	2.3	2.7	2.3	6.4	7.7	2.3	1.4	5.7	3.0	3.0	16.3	17.6	22.2	39.3	1.7	47.54	
2021898_s_at	NM_0249271		swinealpha-neuraminate lyase	3.1	3.3	5.4	8.1	7.2	5.7	5.7	8.8	9.4	37.2	23.4	37.3	39.1	0.6	4.5577		
2222120_s_at	NM_0307691		chromosome 1 open reading frame	3.8	1.2	0.8	1.2	1.4	3.0	4.7	3.2	4.6	20.4	23.6	23.5	18.3	0.6	4.5558		
2021197_x_at	BC0053691		12, clone MGC12484	3.0	2.4	4.3	5.7	5.9	3.3	7.6	7.9	5.4	29.3	32.4	24.3	21.5	1.8	46.33		
2044668_s_at	AL031670		ferritin, light polypeptide-like 1	0.8	0.5	1.8	1.0	1.2	0.3	1.5	1.7	0.9	8.4	8.1	7.0	6.5	1.4	4.614		
20201921_s_at	NM_0041251		quantine nucleotide binding protein 10 (QNL10)	7.1	5.4	2.6	6.7	6.5	11.7	11.4	20.8	15.3	45.5	87.5	81.3	57.1	0.8	2.7	3.0	
2029690_s_at	S661891		peroxisomal alpha-f-coenzyme A oxidase	2.9	1.7	2.8	5.3	4.7	1.4	1.0	1.2	1.3	15.0	17.7	21.4	21.2	0.4	2.1	0.7	
2005119_s_at	NM_0020291		formyl peptide receptor 1	4.1	1.4	1.2	2.6	2.7	1.4	1.1	1.1	4.2	28.2	31.5	24.7	25.9	3.6	1.3	0.7	
21217738_at	BF75514		pre-B-cell colony-enhancing factor	5.7	0.9	7.4	24.1	24.1	7.5	4.6	5.1	0.9	73.4	87.0	83.9	79.9	2.2	1.6	0.7	
2115078_at	AL0503881		DKZp564M422	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.8	0.3	7.1	12.9	45	7.9	0.7	10.1	1.7
20745_s_at	NM_0037441		numb (Drosophila) homolog	0.7	1.4	1.1	2.5	2.4	2.7	1.8	2.9	1.2	7.2	11.2	10.5	7.4	0.8	0.5	1.7	
2121349_s_at	NM_0021551		heat shock 70 kDa protein 6 (HSP70B)	7.7	0.4	0.7	1.5	1.6	2.5	2.8	10.5	17.0	10.4	91.6	70.0	70.8	0.5	1.1	12.8	4.4338
21218023_s_at	NM_0016051		putative nuclearpore protein (LOC51307)	5.7	3.8	6.6	13.0	12.6	8.5	10.3	13.0	10.9	40.1	39.7	47.0	59.7	3.0	44.4	5.9	
2121086_s_at	BC0019061		Similar to metaxin 1	6.2	1.9	2.7	5.4	4.0	1.4	2.2	1.8	3.6	7.4	23.4	23.8	3.6	2.6	4.1	6.0	
20745_s_at	NM_0070743		CD120a, TNFRSF15	1.8	1.5	0.9	1.3	1.4	0.9	1.3	1.6	0.6	85	90	81.1	83.6	65.6	13	4.3118	
203140_s_at	NM_0070761		B-cell CLL lymphoma 6 (BCL6)	6.2	2.9	9.1	13.5	19.8	2.5	16.7	28.7	3.1	99.1	107.8	115.8	101.1	2.2	59	17.4	
20707253_s_at	NM_0165361		ubiquitin 1	3.2	2.3	2.9	4.4	5.0	3.8	2.6	3.8	3.6	16.7	20.0	14.2	17.8	2.3	25	2.4	
202875_s_at	BE97715		pre-B-cell leukemia transcription factor 2	2.0	1.4	0.1	0.1	0.2	2.5	3.6	2.1	1.5	11.6	15.4	6.8	7.5	0.8	1.1	1.3	
2118891_s_at	NM_0247131		FLJ22557	1.2	0.7	2.5	2.7	1.8	0.9	1.5	1.6	1.0	6.9	87	13.2	11.2	1.4	10	0.5	
2118862_x_at	AF0154511		suramin-beta	3.5	2.6	16.8	9.7	10.1	5.6	10.2	7.7	7.1	65.7	67.7	36.1	37.9	3.1	68	8.7	
2117986_s_at	NM_0134481		beta-neurogranin adjacent to zinc finger domain, 1A	3.5	3.0	3.5	9.2	8.4	6.1	8.5	14.5	13.1	39.0	35.1	43.5	51.6	2.5	59	65	
2117956_s_at	NM_0220831		ribon	4.1	1.9	6.4	7.4	9.0	24.2	14.8	25.6	11.8	51.9	105.3	76.2	80.0	0.9	33	3.8	
21126202_at	AB05395		KIAA0933	2.3	3.5	0.4	0.9	1.1	0.8	0.6	0.4	0.8	17.1	18.1	12.9	13.4	1.5	0.5	0.3	
2088485_x_at	NM_0038791		CASP8 and FADD-like apoptosis regulator (CEFLAR)	3.2	2.5	19.2	9.8	9.9	6.2	13.0	8.1	8.3	70.8	69.7	33.8	41.4	3.5	64	8.4	
20942_s_at	FLJ20950		cp 180-carboxypeptidase D-like enzyme	0.6	1.7	0.6	1.3	1.7	1.6	7.0	2.4	26	15.9	23.8	6.8	8.1	0.5	13	2.5	
202933_s_at	NM_0246171		FLJ34019	2.1	2.0	9.6	14.2	14.0	7.1	7.2	10.9	12.5	38.1	37.3	81.5	57.8	19	3.1	4.8	
2027164_s_at	AL574185		glyceral-3-phosphate dehydrogenase 1	6.3	4.4	16.5	18.6	15.0	10.4	15.8	21.9	22.7	80.9	99.2	46.3	60.3	9.5	89	9.4	
2027446_s_at	NM_0066681		Toll-like receptor 6	0.5	0.5	0.7	1.5	0.8	0.8	0.9	1.2	0.8	7.6	11.8	7.2	8.7	0.1	0.9	2.1	
19748_at	NM_0248071		chromosome 6 open reading frame 76	0.2	0.3	0.3	0.4	0.6	1.9	2.6	1.6	1.6	9.1	9.1	6.7	6.4	0.2	0.3	0.5	
20945_x_at	NM_0180501		FLJ10298	1.0	1.4	0.5	0.7	0.7	1.1	0.6	1.5	1.0	80	10.8	13.6	11.0	1.1	0.5	0.3	
212577_at	AA863754		KIAA0650	1.9	1.3	6.4	8.0	9.9	10.1	24.0	8.1	9.4	74.0	98.6	42.2	57.4	44	108	95	
2121732_at	AK026161		Riken cDNA 583040C20	2.8	0.7	3.4	10.5	8.8	5.0	6.0	10.7	10.9	27.6	31.6	30.8	34.7	0.3	0.4	2.5	
05986_at	NM_0049201		apoptosis-associated tyrosine kinase	1.6	1.3	0.7	1.0	0.5	0.3	0.3	1.4	1.0	10.5	15.8	13.3	15.2	32	1.0	0.5	
33501_at	T62985		acyl-Coenzyme A oxidase 1, palmitoyl-sulfatotransferase (STHM)	1.3	1.1	2.0	2.6	2.8	1.3	0.9	1.2	0.6	85	11.5	12.4	7.5	0.1	1.1	0.3	
04542_at	NM_0064561		0.4	0.2	1.5	0.3	0.2	3.4	3.9	0.2	3.4	0.3	32	13.0	13.4	0.7	0.7	0.3	0.3	

## **SUBSTITUTE SHEET (RULE 26)**

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## C. Neutrophil (Ne)-selective transcripts (5/7).

Probe set	Accession #	Transcripts	MC cord	MC blood	Ba1	Ba2	Ba3	Eo	Eo3	Eo4	Ne	Ne3	Ne4	pL	CD4	CD8	CD14	CD19	Fb	NeSL
204071_s_at	NM_005002.1	tumor protein 105/3-binding protein	1.4	7.5	1.1	3.0	2.9	3.7	2.3	2.6	2.05	1.23	8.0	11.9	2.2	2.2	1.4	2.1	40/48	
210594_x_at	AF239756.1	myelin protein zero-line 1	1.2	0.5	0.6	1.5	1.2	0.1	0.4	0.8	1.9	15.3	13.9	7.1	10.9	0.3	0.2	0.6	1.0	39/78
203063_at	NM_014634.1	protein phosphatase 1F (PP2C domain containing)	0.5	0.4	1.4	3.3	3.0	4.0	6.0	6.1	10.0	33.1	22.2	29.6	31.8	0.3	2.9	12	73	15
201392_s_at	BC031974	insulin-like growth factor 2 receptor	1.7	0.7	0.7	0.9	0.1	2.6	3.0	1.9	1.5	51.1	59.1	12.8	15.0	1.1	1.2	4.0	3.8	3.9764
221477_s_at	BT572213	carbohydrate (N-acetyl)glucosamine 6-O-sulfotransferase 7	2.9	1.4	3.4	4.3	9.0	4.2	4.2	4.2	4.2	56.8	63.6	36.1	46.6	7.9	32	1.2	12.6	27
205756_at	NM_019886.1	myxovirus (influenza) resistance 2 (MX2)	0.2	0.1	0.1	0.0	0.1	0.1	0.1	0.1	0.1	5.0	3.9	3.5	10.5	0.1	1.3	1.0	1.0	0.2
204994_at	NM_002463.1	cathepsin peptidase D	1.3	2.3	5.4	7.8	8.2	9.2	11.6	15.2	12.3	49.8	46.6	77.6	80.8	2.4	7.5	6.0	15.6	48
201942_s_at	NM_0013042	CD55 fas/APO-1	0.9	0.9	0.5	2.1	3.6	1.7	7.6	7.2	4.6	16.4	21.3	18.7	15.2	0.7	1.0	1.7	3.3	0.4
216252_x_at	Z70519.1	B cell RAG-associated protein	0.3	0.8	4.3	2.5	1.1	1.8	4.7	1.8	1.7	18.5	31.2	10.3	8.4	2.2	3.8	24	1.9	1.4
203066_at	NM_014863.1	FJ_3910	1.3	3.9	0.9	12	1.0	10.6	10.2	13.1	20.2	57.0	65.9	95.2	86.9	1.9	0.1	0.0	19.3	42
212479_s_at	AL050139.1	recapin	1.7	1.6	2.1	2.1	2.6	2.4	2.5	3.5	1.7	9.0	10.1	8.8	9.8	1.1	2.3	2.4	22	19
209371_at	U03644.1	Casp8 and FADD-like apoptosis regulator	0.7	0.2	1.6	2.3	2.7	2.2	1.3	2.6	2.7	6.8	7.8	12.8	10.9	0.8	1.0	1.1	1.2	1.5
211317_s_at	AF041461.1	C-type calcium-dependent carbohydrate-recognition domain lectin superfamily member 2	1.6	1.8	9.5	3.6	4.0	3.7	6.8	3.2	2.8	33.1	44.8	15.2	17.6	2.4	4.7	6.5	5.7	4.9
209732_at	BC005254.1	clone 24450 RING zinc finger protein R2F	8.1	5.9	10.0	18.6	23.6	9.0	10.0	8.9	7.3	72.9	77.0	99.7	75.5	4.1	14.4	21.2	10.2	16.4
201779_s_at	AF070558.1	KIAA0232	1.2	1.4	0.9	0.2	0.2	1.1	5.2	0.7	1.4	33.1	26.7	27	4.0	0.3	0.1	0.4	2.6	0.1
212441_at	D89852	solute carrier family 6, member 6 (SLC6A6)	0.7	0.7	2.3	3.6	3.0	1.2	1.2	1.1	1.2	10.6	10.9	12.5	9.9	2.2	1.1	2.0	15	0.7
205920_at	NM_003043.1	DKFZp786A181	1.48	5.9	13.0	13.3	13.9	21.8	27.0	25.3	13.1	88.2	108.1	116.5	81.8	6.0	9.6	11.3	25.7	15.7
213396_at	AL050391.1	cathepsin-like apoptosis regulatory protein (casp)	5.4	2.9	3.5	9.8	10.3	8.0	6.9	11.5	11.3	31.9	30.1	30.8	49.8	2.5	2.0	4.0	5.9	2.1
209508_at	AF05774.1	FJ_10604	1.7	2.7	10.8	7.6	11.5	4.9	6.3	6.0	8.4	37.0	34.8	34.7	40.8	2.7	4.0	5.1	6.3	3.4
218115_at	NM_018154.1	FLJ_43320	0.9	2.2	2.4	1.5	0.9	1.8	2.1	1.3	1.1	10.5	9.1	6.7	7.7	1.1	1.2	2.2	2.1	3.7451
215652_at	AK024821	RAF65 interacting protein 1	0.2	0.1	2.0	0.3	1.6	0.3	0.3	1.2	0.7	55	45	34	25	0.1	0.3	1.0	0.9	0.2
212061_at	AA49595	KIAA0963	1.00	6.1	10.2	12.4	11.4	18.7	14.9	12.1	10.0	66.3	60.0	47.6	37.1	4.0	8.7	9.9	13.9	3.7615
221874_at	AB037745.1	KIAA1324	0.3	0.3	0.7	1.1	0.1	1.0	1.3	0.1	0.8	11.8	12.5	4.0	29	0.3	0.9	1.7	1.2	3.6962
217207_s_at	AK025671	butyrophilin-like receptor	1.2	1.7	1.4	2.1	1.7	1.2	1.9	0.6	0.6	24	10.9	34	7.2	6.1	1.5	1.6	0.9	1.3
212579_at	AA868754	IL-1 receptor antagonist IL-1Ra (IL-1RaN)	1.3	1.6	5.3	9.8	15.5	7.3	7.8	11.3	8.3	32.8	42.9	40.0	39.7	2.0	5.4	5.7	31	105
212657_s_at	AM083357	phosphotyrosine decarboxylase	4.88	2.3	0.9	0.5	0.6	2.1	0.9	1.5	1.3	35.2	37.0	48.2	35.5	0.6	0.3	9.3	0.4	0.6
202392_s_at	NM_014238.1	arginase (Arg)	3.4	2.7	6.2	11.7	6.8	3.4	4.7	5.4	4.7	32.8	31.0	22.0	32.3	0.8	1.6	4.2	1.4	12
206177_s_at	NM_000452	IL5-induced IFN- $\alpha$ factor (IFC)	0.5	1.3	2.2	0.4	0.6	0.9	0.8	0.7	0.7	3.9	4.3	8.1	5.0	1.1	0.1	0.4	0.6	0.7
200706_s_at	NM_004962.1	FLJ_3910	31.2	39.0	20.7	64.6	62.5	15.6	13.4	31.8	217	1732	148.5	1720	150.2	85	13.3	42.7	143	167
212478_at	AL050391	cytostatin	0	0	0.7	0.2	2.3	35	1.4	0.8	1.5	1.0	3.7	3.0	4.8	6.65	0.1	0.3	1.1	0.6
218860_at	NM_003045.1	exportin 6	2.5	0.5	1.5	0.2	0.2	1.7	0.2	2.6	1.1	48.5	51.8	44.5	20.4	33	1.2	1.7	106	0.5
211982_x_at	AL546600	glutamate binding protein 2	9.8	6.7	14.9	31.8	27.8	24.6	24.0	34.0	24.0	107.2	101.1	86.6	90.2	66	75	174	96	115
202748_at	NM_0041202	intereron-inducible (GBP2)	2.4	5.3	3.7	9.0	7.4	3.3	2.1	3.0	3.3	28.1	35.2	45.0	24.8	42	7.3	90	6.3	3.6111
220088_at	NM_001736.1	GPR	22	23	15.4	24.6	24.8	17.1	15.6	9.8	12.0	90.5	104.5	84.4	91.1	23	1.2	0.5	25.6	10
202890_at	T62571	Cs receptor	0.9	0.1	0.7	1.4	1.1	0.1	0.0	0.2	0.1	25	31	32	7.1	0.0	0.7	4.8	11.1	0.4
220987_s_at	NM_030952.1	microtubule-associated protein 7 (DKZP434037)	14	0.3	3.9	4.9	4.7	9.6	9.3	14.1	11.7	43.0	35.6	57.8	57.6	53	4.7	4.8	11.1	3.5748

Fig. 6H

## C. Neutrophil (Ne)-selective transcripts (6/7).

Probe set	Accession #	Transcripts	MC blood	MC cord	MC lung	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3	Eo 4 (small)	Ne 1	Ne 2 (small)	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	NeSL1
20707_at	NM_003893.1	interleukin 18 receptor accessory protein (IL18RAP) CD95, Fas, Apo-1	5.9 1.0	0.9 0.6	2.2 3.1	3.4 2.7	4.1 1.6	7.2 2.2	1.6 5.2	2.8 1.8	1.7 1.7	13.4 19.0	9.7 31.9	20.9 11.4	5.6 9.4	24 1.0	2.8 4.5	3.1 2.2	0.4 1.6	0.4 1.1	1.6 4.4	0.3 0.3	35722 35657
215719_X_at	X3493.1	R	4.9	1.2	2.6	5.0	3.7	0.7	0.1	2.1	0.7	28.5	31.8	34.8	33.8 0.3	1.2 1.2	1.9	9.0	6.5	0.3	3.563		
218404_at	NM_013322.1	sorting nexin 10 phosphatidylycerophosphate synthase (PGS) KIAA0690	3.4 0.1	3.0 0.3	1.7 0.1	4.2 0.1	3.5 0.1	24 1.9	3.8 2.5	6.1 2.3	9.2 1.1	17.2 8.9	16.9 8.3	17.5 7.5	16.3 10.9	1.0 0.1	2.1 0.1	2.6 0.2	24 25	1.5 0.1	1.7 0.0	35544 35402	
219394_at	NM_024491.1	formylpeptide receptor 1 FLAME-1-delta KIAA0134	1.4 1.4	1.5 1.5	5.3 5.3	6.6 7.0	4.3 4.2	5.9 3.5	42 21.2	35 30.3	42.7 18.4	43 19.6	15.8 21	42.5 29	46 40	1.7 1.9	6.2 6.2	1.7 1.7	0.9 0.9	1.7 1.7	0.9 0.9	3.5148 3.5148	
216913_S_at	AK01460.1	GPR	1.3	1.3	2.9	2.0	1.7	8.7	15.8	35	43 42.7	42.5 46	15.3 15.3	0.6 0.6	1.3 1.3	1.9 1.9	6.2 6.2	1.7 1.7	0.9 0.9	0.9 0.9	3.5148 3.5148		
205118_at	M60562.1		0.9	0.6	0.7	0.1	0.3	0.2	0.4	0.8	0.7	6.1	6.4	4.6	4.6	0.2	0.3	0.2	0.1	0.6	0.5	0.1	35126
210564_X_at	AF098619.1		0.9	0.6	0.7	0.1	0.3	0.2	0.4	0.8	0.7	6.1	6.4	4.6	4.6	0.2	0.3	0.2	0.1	0.6	0.5	0.1	35126
210607_X_at	BE51347		0.9	0.6	0.7	0.1	0.3	0.2	0.4	0.8	0.7	6.1	6.4	4.6	4.6	0.2	0.3	0.2	0.1	0.6	0.5	0.1	35126
203688_at	NM_002361.1	thrombomodulin interleukin-1 receptor accessory protein (IL1RAP)	0.5	0.1	0.0	0.1	0.6	0.8	0.4	0.6	0.7	1.8	3.0	2.0	2.3	0.6	0.0	0.0	0.0	0.0	0.0	0.3	35023
210233_at	AF167243.1	myeloid cell nuclear differentiation antigen	1.2	0.6	2.42	5.0	26.2	17.5	17.9	49.8	22.3	29.8	29.02	186.0	217.0	34	1.5	0.6	66.6	25	0.0	3.4903	
204959_at	NM_002432.1	riban	6.3	3.7	16.3	42.4	35.9	27.9	29.5	43.0	30.9	107.4	115.3	117.9	110.3	2.6	7.5	9.9	49	34	20.4	3.4847	
217957_at	AF288391.1		0.8	1.5	1.9	4.6	5.5	5.5	6.9	9.9	9.0	28.3	32.9	34.0	42.7	1.7	3.7	4.1	5.1	9.8	3.0	3.4777	
221763_S_at	A1694223																						
207857_at	NM_0068866.1	R	0.4	0.5	3.6	8.5	5.3	4.5	4.9	1.6	6.3	33.5	34.3	46.2	50.8	1.8	0.0	0.1	11.6	0.5	0.1	34773	
220740_S_at	NM_0051351	solute carrier family 12 member 6 (SLC12A6)	1.6	1.0	2.5	3.3	3.4	3.5	5.6	3.2	32	12.6	19.0	107	144	4.0	2.9	2.2	2.9	3.5	0.8	34722	
217739_S_at	NM_005746.1	pie-8-cell colony-enhancing factor	7.1	1.7	5.9	46.0	61.0	18.9	13.9	12.9	9.3	11.4	12.0	90.8	93.4	1.2	2.3	1.4	17.6	2.1	3.1	3.4242	
205941_S_at	NM_000607.1	oncosinucleotid 1 (CRN1)	0.3	1.0	0.4	0.1	0.1	0.0	0.1	0.1	0.1	2.6	3.6	2.7	0.4	0.1	0.2	0.1	0.5	0.0	0.1	3.4189	
214784_X_at	BE566299	exopin 6	7.4	5.0	10.0	23.7	23.9	13.0	16.7	23.3	20.5	60.3	67.8	57.2	60.8	2.9	8.7	7.8	6.6	5.9	5.4	3.4155	
217985_S_at	AA102574	beta-domain adjacent to zinc finger domain, T4	1.5	1.4	1.8	2.6	3.8	7.4	5.1	7.3	4.7	16.9	19.2	22.1	24.2	2.7	2.5	2.3	3.5	2.4	0.9	33999	
212598_at	A1806395	KIAA093	0.7	0.7	0.7	0.1	0.1	0.1	0.1	0.1	0.1	5.5	7.3	3.1	3.2	0.2	0.1	0.1	0.1	0.1	0.1	33933	
219053_S_at	NM_017966.1	FLJ20847	2.6	2.0	1.9	2.3	2.3	2.6	2.1	3.0	2.8	11.3	7.6	22.2	34.1	1.6	0.5	0.9	4.7	1.3	2.9	33686	
217475_S_at	AC002073	PAC clone RP3-515N1	0.6	0.5	0.6	0.2	0.4	1.3	1.3	0.5	1.2	5.9	9.8	1.6	1.4	0.7	0.3	0.1	0.5	0.7	0.2	33448	
463323_at	AL120741	Caz2-dependent endoplasmic reticulum nucleoside diphosphatase	4.4	3.2	4.2	8.3	7.2	5.3	6.7	11.4	7.9	20.0	21.5	33.9	26.3	2.5	2.8	3.6	43	34	5.0	33028	
201955_S_at	NM_015046.1	KIAA0625	0.5	0.1	3.7	3.0	4.0	4.8	4.9	2.7	5.8	18.8	23.4	6.8	20.6	1.6	0.1	2.8	2.4	2.0	3.5	33019	
203628_at	NM_000875.2	R	1.8	1.5	1.9	5.6	5.6	6.4	4.8	11.3	8.9	17.0	20.5	36.5	28.2	0.1	1.1	1.1	0.6	0.5	0.8	32887	
202193_at	NM_0055692	LIM domain kinase 2 (LIMK2)	0.5	0.1	2.9	63	72	45	4.0	4.7	4.9	13.2	17.0	18.1	24.0	1.2	2.5	2.2	3.9	3.0	5.4	32887	
203042_at	NM_002294.1	lysosomal-associated membrane protein 2 (LAMP2)	1.9	1.4	0.8	1.5	1.3	3.1	2.7	3.8	21	42.1	42.2	27.0	25.1	2.7	0.9	0.5	10.2	0.4	0.2	32526	
22026_S_at	NM_018071.1	FLJ10357	0.0	0.8	0.2	0.0	0.4	0.2	0.1	0.1	0.0	3.8	3.7	3.1	5.6	0.2	0.1	0.1	0.0	1.2	0.7	32404	
212470_at	AB011088.1	spemn-associated antigen 9	0.2	0.1	0.8	0.7	1.2	0.7	0.9	0.9	0.6	3.3	3.2	4.2	29	0.0	0.3	0.2	1.0	0.1	0.3	32282	
203433_at	NM_006441.1	clone 6 immunoglobulin-like transcript 5	1.4	1.8	1.5	2.5	1.6	3.1	4.2	3.5	3.1	15.8	11.4	9.6	9.0	1.6	1.8	1.9	2.9	1.7	1.5	32181	
214486_X_at	AF041459.1	DKZP2340328	1.9	2.1	10.7	5.0	6.5	4.2	5.3	4.3	6.0	26.3	16.2	25.3	24.2	2.4	3.7	5.0	5.3	2.3	1.9	32114	

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Fig. 6I

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## C. Neutrophil (Ne)-selective transcripts (7/7).

Probe set	Accession #	Transcripts	MC <sub>cord</sub> blood	MC <sub>lung</sub>	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Eo 1 (small)	Eo 2 (small)	Eo 3 (small)	Eo 4 (small)	Ne 1 (small)	Ne 2 (small)	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba S.I.	
209222_s_at	BC000961	oxysterol binding protein-like 2	1.3	0.2	27	88	80	54	54	77	73	172	184	223	239	0.9	23	34	28	20	13	3.1877	
202334_s_at	AA877765	ubiquitin-conjugating enzyme E2B mitogen-activated protein kinase 4	3.3	3.4	48	155	121	53	72	147	128	209	256	436	381	40	45	39	39	25	4.9	4.6	3.1877
203266_s_at	NM_003010.1	TRAF and TNF receptor-associated protein (ADAM22) transmembrane	3.7	2.4	49	82	63	25	48	68	50	147	152	274	269	28	24	26	27	23	27	3.1804	
58780_s_at	R42449	LM domain kinase 2	4.5	5.4	15	3.9	3.0	7.8	9.6	12.8	16.4	28.0	27.6	46.7	44.1	1.2	0.6	0.1	6.5	6.5	0.2	5.7	3.1803
210582_s_at	AL17466.1	ELYS transcription factor-like protein TMB362	3.8	1.9	43	5.1	4.8	8.7	10.3	10.8	9.4	33.9	36.5	30.8	23.8	1.3	1.7	1.8	1.9	0.9	1.4	3.1609	
214766_s_at	AL080144.1	TRAF and TNF receptor-associated protein (ADAM22) (HDA2) complex (80 kDa)	1.3	0.2	2.0	3.1	4.2	1.9	1.4	2.1	2.4	9.4	9.5	9.9	11.3	3.2	1.3	0.8	0.5	1.0	1.3	3.1414	
202266_at	NM_016614.1	transmembrane	9.8	6.2	94	23.7	20.9	86	99	16.5	14.0	36.1	56.5	64.5	57.5	45	7.7	9.4	5.3	8.2	6.3	3.1402	
203278_s_at	NM_006621.1	gamma-carboxyglutamic acid protein 4	2.1	2.8	27	14.8	11.0	5.7	5.0	7.4	4.9	21.0	16.6	31.0	30.6	0.7	3.0	4.5	3.1	2.7	3.0	3.1882	
207291_at	NM_024081.1	Dicer, Dcr-1 homolog (Drosophila) solute carrier family 31 (SLC31) ornithine decarboxylase antizyme clone 17.6 immunoglobulin-like transcript	0.5	1.2	1.3	1.4	1.4	1.1	0.9	0.2	0.4	0.2	3.8	7.9	4.5	8.5	0.2	0.8	0.1	1.9	1.1	0.4	3.1336
213229_at	BF59031	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN) hypophosphorylated	0.5	4.5	19.5	12.9	15.4	15.9	97	19.1	16.0	35.2	3.9	61.4	62.0	5.9	7.3	1.2	2.2	1.2	1.2	1.2	3.1316
204204_at	NM_001360.1	major histocompatibility complex, class I, B, regulator of pigmentoase GTpase interacting protein 1 (RGP1)	1.7	1.7	7.3	4.4	2.3	0.8	1.7	0.9	2.3	1.2	22.6	23.8	31.3	36.0	0.2	0.2	0.2	0.2	0.2	0.2	3.1262
203164_s_at	AF24221.1	toll-like receptor 2 (CD28, FcγR-1, KIAA0993)	8.3	7.3	44	22	1.9	11.5	21.9	8.0	7.7	61.9	59.1	21.0	27.7	22	22	5.1	6.3	12.2	6.2	9.6	3.1253
210784_x_at	AF00934.1	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN) hypophosphorylated	1.4	0.1	2.1	1.2	2.4	2.5	2.2	2.8	2.1	52.1	48.8	31.8	36.3	0.8	0.2	0.2	13.3	0.3	0.2	3.1236	
202625_at	A1356412	immunoglobulin superfamily, member 6 (IGSF6)	6.9	6.9	5.0	18.2	14.9	20.7	21.7	27.7	28.6	74.7	76.3	77.5	75.7	7.5	7.7	0.9	17.1	23.6	0.5	3.1131	
221895_at	AW469184	FLAME-1	2.2	0.5	5.4	5.2	5.8	5.2	3.4	7.6	5.1	14.8	12.0	24.6	19.2	2.0	2.4	2.1	5.2	1.5	1.6	3.1131	
37384_at	D13640	intercellular adhesion molecule 3 (ICAM3)	2.5	3.0	3.4	3.8	3.8	6.7	6.6	7.6	6.6	25.2	17.9	21.3	29.4	2.6	2.5	2.5	7.4	1.8	2.8	3.0985	
206608_s_at	NM_020366.1	complement C1r subcomponent	1.1	1.4	1.2	0.8	1.0	1.1	1.0	0.5	1.4	6.1	3.4	5.3	4.7	1.5	0.9	0.8	1.3	0.5	0.7	3.091	
204924_at	NM_003764.1	CD14, FcγR-1, R	1.8	0.7	1.1	5.9	8.2	2.8	0.4	0.8	1.4	52.9	88.0	94.4	99.8	1.6	1.3	0.7	0.9	0.4	0.9	3.0909	
204918_s_at	NM_000433.1	CD95, FcγR-1, R	2.0	2.0	5.9	11.0	8.9	5.4	4.4	6.8	7.0	20.6	27.1	27.0	29.1	0.3	5.2	5.3	4.0	2.0	3.8	3.0927	
212606_at	AI806395	CD28, FcγR-1, R	3.1	2.9	20.1	19.4	31.9	11.6	11.9	20.6	19.1	58.8	74.1	72.8	81.0	0.1	0.2	0.3	6.6	0.0	3.4	3.097	
211316_X_at	AF009616.1	CD28, FcγR-1, R	4.4	2.5	3.2	6.4	4.8	10.7	9.7	18.5	12.1	29.3	34.1	44.7	46.1	0.5	1.2	1.7	8.3	0.2	2.9	3.0746	
204949_at	NM_0021622	CD28, FcγR-1, R	3.0	3.7	5.7	46.3	34.5	38.9	51.6	94.5	93.7	161.1	168.3	239.1	241.1	4.5	13.6	21.0	17.6	199	13	3.0617	
206208_at	NM_007172	CD28, FcγR-1, R	2.2	0.6	0.7	0.7	0.7	0.7	0.7	1.0	0.8	56	52	28	24	1.2	0.7	0.7	0.7	0.7	0.7	3.0572	
213227_X_at	AI743654	CD28, FcγR-1, R	2.1	1.7	5.0	15.0	12.1	8.9	13.7	25.4	23.9	49.9	28.3	59.9	75.8	0.7	4.5	6.6	5.7	5.4	3.7	3.0554	
202626_s_at	NM_002350.1	CD28, FcγR-1, R	15.5	9.5	12.1	12.7	14.8	32.6	31.6	54.0	41.0	110.1	115.1	122.7	127.2	18.4	21	1.5	36.8	33.0	0.6	3.0541	
206420_at	NM_005849.1	CD28, FcγR-1, R	1.1	1.3	0.2	0.4	0.7	1.9	1.2	1.1	1.0	17.5	24.2	30.6	33.3	1.4	0.4	0.4	8.4	0.3	0.3	3.0442	
201651_s_at	NM_007229.1	CD28, FcγR-1, R	21.4	17.4	4.6	24.8	20.1	13.3	19.5	33.9	35.3	61.3	72.5	76.1	94.4	24.7	4.9	4.4	8.6	6.1	8.0	3.0391	
219540_at	AU150728	CD28, FcγR-1, R	2.0	1.0	1.3	3.7	3.6	20	15	4.4	3.7	6.7	6.9	9.2	9.9	1.0	2.1	1.3	1.0	1.6	0.1	3.0361	
201244_s_at	NM_002880.1	CD28, FcγR-1, R	6.0	5.4	12.4	32.8	33.1	14.9	19.0	27.3	25.7	60.4	58.2	89.2	86.2	22	6.6	11.3	12.8	7.6	7.3	3.0329	
203365_s_at	AA810268	CD28, FcγR-1, R	1.4	1.2	2.8	6.4	4.5	1.7	2.6	3.5	3.1	12.8	12.8	10.4	16.8	1.4	1.4	1.3	1.3	1.3	2.5	1.5	
203030_s_at	AF007555.1	CD28, FcγR-1, R	0.0	0.0	16	12	0.1	0.1	0.1	0.1	0.8	30	1.1	2.8	0.1	0.1	0.0	0.0	0.1	0.5	0.5	3.028	
203739_at	NM_006526.1	CD28, FcγR-1, R	1.9	2.6	3.0	18.4	8.4	7.6	8.0	14.7	14.9	37.3	45.1	24.4	27.0	1.2	4.6	5.3	6.1	5.5	3.6	3.0558	
204747_at	NM_0015491	CD28, FcγR-1, R	2.0	3.0	4.9	6.0	3.5	4.3	12.4	4.4	3.0	24.2	27.0	15.4	12.0	0.3	1.8	1.2	6.2	1.4	2.6	3.0143	
206209_s_at	NM_0007172	CD28, FcγR-1, R	0.7	1.0	0.8	0.6	0.6	2.2	2.1	1.5	2.1	13.8	7.4	4.7	3.5	2.7	1.0	0.5	0.5	1.0	0.5	3.0143	

## **SUBSTITUTE SHEET (RULE 26)**

#### **D. Mast cell (MC)-selective transcripts (2/2).**

Probe set	Accession #	Transcripts	MC												MC															
			cord blood	MC lung	MC Ba 1 (small)	MC Ba 2 (small)	MC Ba 3 (small)	MC Ba 4 (small)	MC Ba 5 (small)	MC Ba 6 (small)	MC Ba 7 (small)	MC Ba 8 (small)	MC Ba 9 (small)	MC Ba 10 (small)	MC Ba 11 (small)	MC Ba 12 (small)	MC Ba 13 (small)	MC Ba 14 (small)	MC Ba 15 (small)	MC Ba 16 (small)	MC Ba 17 (small)	MC Ba 18 (small)	MC Ba 19 (small)	MC Ba 20 (small)						
207480_s_at	NM_020149.1	TALE homeobox protein Meis2	14.0	14.9	1.9	3.6	4.0	1.7	1.9	5.3	3.8	0.3	0.6	1.0	0.3	0.5	0.8	0.4	0.6	0.4	0.8	0.2	0.1	0.1	0.8					
45288_s_at	AA209239	lipase	10.9	3.0	0.2	2.1	0.8	0.5	0.5	1.3	0.9	0.1	0.1	0.2	0.7	0.4	0.5	0.5	1.3	1.0	0.9	0.52869								
207039_at	NM_000077.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	7.5	3.6	0.7	0.7	0.1	0.6	0.4	0.3	0.5	0.1	1.2	0.6	1.1	0.1	0.9	0.5	0.8	0.1	1.2	4.35629								
201650_at	NM_002276.1	keratin 19	6.2	12.0	0.0	0.0	0.3	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.1	0.1	0.0	0.1	0.1	0.1	0.0	0.0	0.1	0.0	0.1	0.0				
214533_at	NM_001836.1	chymase	10.1	2.7	0.4	0.2	0.8	0.1	0.1	0.8	0.6	0.1	0.1	0.2	0.2	1.2	0.7	0.5	1.0	0.4	0.3	4.27984								
218211_s_at	NM_024101.1	melanophilin	24.8	29.6	2.7	2.5	1.8	3.0	2.5	1.9	2.2	4.6	4.1	3.3	4.1	6.4	4.0	3.2	2.4	3.4	2.7	4.24499								
203916_at	NM_003635.1	N-deacetylase/N-sulfotransfase	17.9	26.7	3.2	6.5	6.8	2.5	2.7	3.6	3.7	4.2	3.4	5.5	5.2	0.9	3.1	4.9	3.3	2.7	2.4	4.20693								
2102336_at	AB002336.1	erythrocyte membrane protein band 4.1-like 1	3.8	6.4	0.1	0.2	0.1	0.5	0.1	0.2	0.4	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.4	0.1	0.2	0.4	0.1	0.2			
200766_at	NM_001909.1	cathepsin D	42.6	39.5	2.5	5.3	4.3	4.8	3.4	2.7	4.0	6.7	3.1	1.9	2.6	1.6	2.5	1.0	1.6	2.5	10.0	1.6	5.9	4.1037						
2022118_s_at	NM_004265.1	delta-6-fatty acid desaturase (FADS6)	18.8	24.5	0.4	0.2	1.0	0.3	0.1	0.8	0.5	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.6	0.1	0.6	0.1	0.5	4.08548		
204066_s_at	NM_014914.1	centaurin, gamma 2	5.3	7.9	0.4	0.4	0.7	0.2	0.6	0.6	0.3	0.5	0.4	0.4	0.8	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	4.06712		
209644_x_at	U38945.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) lipoate	14.0	6.4	1.0	1.4	0.7	1.2	1.3	1.7	1.5	1.0	1.6	1.5	2.1	2.3	1.8	1.5	0.9	0.3	24.388459									
221679_s_at	AF225418.1	heat shock protein 70 kD	2.8	1.9	0.4	0.9	0.1	0.3	0.4	0.4	0.1	0.1	0.5	0.0	0.5	0.5	0.7	0.6	0.6	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	3.83039		
211538_s_at	U56725.1	4.4	7.4	0.3	0.6	0.4	0.6	0.3	0.3	0.9	1.4	0.4	1.0	0.8	1.5	0.5	0.5	0.5	0.1	0.5	0.5	0.1	0.5	0.5	0.1	0.5	3.80423			
211548_s_at	J05594.1	82.6	60.0	19.4	26.0	16.3	32	29	18	1.7	0.8	0.5	0.9	0.2	4.1	12	0.9	0.1	0.6	0.2	0.6	0.2	0.6	0.2	0.6	0.2	3.49258			
210174_at	AF228413.1	RAB38, member RAS oncogene nuclear receptor subfamily 5, group A, member 2	2.9	3.4	0.5	0.5	0.6	0.8	1.1	0.7	1.2	1.1	0.4	0.1	0.4	0.9	0.7	0.2	0.2	0.6	0.3	3.47124								
219412_at	NM_022337.1	3.9	4.0	0.1	0.4	0.3	0.7	0.1	0.2	0.3	0.2	0.2	1.1	0.1	0.1	1.2	0.1	0.8	0.4	0.1	0.5	3.32805								
211850_at	NM_001747.1	70.5	64.5	9.6	30.8	28.8	8.1	7.8	11.5	9.9	2.6	3.6	3.0	24	1.6	1.1	1.0	17.0	58	53	3.29919									
205888_s_at	AF956693	KIAA0555	5.4	4.6	0.7	1.6	1.2	0.8	0.7	0.1	1.0	1.3	0.3	0.2	0.6	1.2	0.3	1.5	0.7	1.2	0.4	3.25597								
221750_at	BG035985	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	5.0	3.8	0.9	1.5	1.1	1.1	1.2	1.3	1.0	1.3	0.5	0.7	1.2	0.7	0.5	1.1	0.9	0.3	0.6	0.8	0.4	0.3	0.5	0.4	3.1926			
214218_s_at	AI699347	nuclear receptor subfamily 1, group I, member 3	3.5	3.5	0.7	0.6	0.7	0.5	2.2	0.5	0.7	1.2	0.6	0.1	0.1	1.1	0.9	0.3	0.6	0.8	0.4	0.3	0.5	0.2	0.2	0.2	0.3	3.07851		
218807_s_at	NM_015385.1	FLJ21080	16.1	23.7	0.5	2.3	2.5	0.9	1.1	2.7	2.1	1.1	0.8	0.8	0.9	2.3	2.1	2.9	0.6	2.0	63	3.07851								
221577_s_at	AF039341	SH3-domain protein 5 (ponsin)	1.4	1.9	0.4	0.9	0.4	0.5	0.0	0.0	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.2	0.2	0.2	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	3.07366	
355820_at	X62078	prostate differentiation factor	21.8	55	0.6	0.3	0.5	0.6	0.1	0.2	0.6	0.0	0.2	0.3	0.1	0.1	0.2	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	3.05532		
203744_s_at	BG403660	GM2 activator protein	7.3	176	1.4	3.3	1.3	0.3	0.2	0.5	0.5	0.8	1.9	0.3	0.4	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.1	0.1	0.1	0.1	0.1	5.0	2.7	3.01647
		heat shock 105 kD																											0.9	20.30067

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## **SUBSTITUTE SHEET (RULE 26)**

Fig. 6L

### E. Basophil and eosinophil-selective transcripts (1/1).

## **SUBSTITUTE SHEET (RULE 26)**

Fig. 6M

## E. Eosinophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC. blood	MC. lung	Ba 2 (small)	Eo (small)	Eo 3 (small)	Eo 4 (small)	Ne (small)	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	EO-NeSI.				
221345_at	NM_005306.1	GPR GPR43/PAR1-like zinc finger DHHC domain containing 18	0.1	0.4	0.9	0.6	0.6	0.7	16.6	15.4	10.5	49.7	45.7	22.5	23.0	0.8	0.1	0.7	21.742			
212860_at	BG163720	solute carrier family 19 member 1	2.2	0.8	4.1	3.9	4.0	16.0	17.4	14.8	16.7	59.2	53.9	30.9	39.8	1.1	2.4	2.6	1.5	1.3		
211576_s_at	BC003068.1	nephroblastoma overexpressed gene ARF-GAP, RHO-GAP, ankyrin repeat and pleckstrin homology domains-containing protein 3	1.4	0.1	0.7	1.4	0.7	5.1	5.9	11.5	12.4	19.8	18.7	27.1	28.1	1.8	0.9	0.4	2.7	0.5	0.8	
214321_at	BF44025	1.3	1.0	0.8	0.2	0.7	6.2	7.2	17.0	13.7	4.5	7.6	10.7	11.3	0.1	0.1	0.0	0.1	0.1	1.8		
218950_at	NM_022481.1	BCL2-related protein A1	1.4	3.1	24	3.7	2.1	15.5	15.9	18.3	15.5	28.0	24.3	15.9	20.6	0.7	0.2	0.8	3.9	0.9	1.0	4.829
205681_at	NM_004049.1	granulin CDNA FLJ36416, clone	0.5	1.9	1.0	3.2	24	52.4	40.2	35.9	30.5	46.5	49.2	35.5	33.5	1.5	2.2	1.9	8.3	4.3	0.2	4.7782
203765_at	NM_012198.1	THYMU2011053	2.0	1.8	4.5	11.7	8.3	27.5	39.8	46.7	34.8	71.6	85.2	80.5	77.9	1.0	1.2	12.1	3.1	0.5	4.4403	
213241_at	AF033307.1	hypothetical protein PRO831	5.0	2.4	1.6	1.0	1.0	33.2	37.1	68.7	40.6	63.2	77.8	89.2	80.9	3.0	3.0	2.8	13.5	4.1	7.8	4.2603
221815_at	BE671816	homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2	1.2	1.4	1.3	0.5	1.6	10.1	8.8	11.2	6.4	5.0	6.2	4.0	3.8	1.6	0.8	0.2	1.4	0.9	0.6	4.1325
214153_at	BE467941	KIAA0559	1.0	0.6	1.0	2.0	3.1	9.1	10.4	18.2	16.6	9.7	9.7	14.5	15.2	0.8	0.9	1.2	0.7	2.3	0.1	4.0797
212821_at	AU147160	Edg4, endothelial differentiation lysophosphatidic acid G-protein-coupled receptor 4	0.1	0.1	0.4	1.2	0.9	4.6	2.8	4.7	3.4	4.4	3.5	6.0	7.9	0.4	0.2	0.4	0.3	0.0	0.2	3.727
206723_s_at	AF011466.1	adenosine monophosphate deaminase 2 (sotomyl)	1.2	1.4	2.1	3.6	2.6	13.7	8.0	19.6	22.3	24.6	17.0	26.1	29.1	0.1	3.6	5.0	3.8	1.9	0.9	3.7119
212360_at	A1916249	transforming acidic coiled-coil containing protein 3 (TAC3)	1.0	2.0	2.6	5.9	4.6	26.6	18.7	30.2	31.9	78.7	63.1	79.5	91.3	3.4	5.8	6.1	12.6	3.7	5.8	3.5888
218308_at	NM_006342.1	protein kinase C-like 2	0.4	0.4	4.8	8.3	9.5	33	24	33	4.7	17.6	14.8	23.5	22.8	24	2.3	1.6	3.6	1.0	0.7	3.4769
212679_s_at	AK023692.1	serum glucocorticoid regulated kinase (SGK)	1.9	0.6	3.1	3.7	5.1	11.8	7.6	17.7	13.8	16.7	23.6	27.0	28.4	1.1	2.1	2.2	4.2	4.2	2.9	3.2963
201739_at	NM_005627.1	ectonucleotide triphosphate diphosphorylase 1	30.2	25.2	1.9	18.5	25.4	114.1	116.0	150.9	164.8	60.2	77.1	105.8	156.3	1.1	3.7	0.7	34.6	16.189	32456	
209473_at	AV717590	growth arrest and DNA damage inducible protein beta (GADD45B)	1.4	0.6	2.1	1.6	2.0	15.9	22.3	39.5	29.1	14.1	13.7	23.7	13.8	2.6	1.3	6.5	4.8	0.6	3.0752	
209304_X_at	AF087853.1	iduronate 2-sulfatase	0.1	0.3	1.3	0.5	1.7	7.1	2.9	3.3	3.8	6.1	5.1	5.2	10.8	0.4	0.1	0.9	0.7	0.4	0.1	3.0295
210666_at	AF050145.1																				3.0005	

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## **G. Basophil and neutrophil-selective transcripts (1/1).**

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3.18834  
3.1591

Fig. 60

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## H. Mast cell and basophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC <sub>cord</sub>		MC <sub>blood</sub>		Ba 1 (small)		Ba 2 (small)		Eo 1 (small)		Eo 3 (small)		Eo 4 (small)		Ne 1 (small)		Ne 2 (small)		Ne 3 (small)		Ne 4 (small)	
			lung	MC	lung	MC	lung	MC	lung	MC	lung	MC	lung	MC	lung	MC	lung	MC	lung	MC	lung	MC	lung	MC
205624_at	NM_001870.1	carboxypeptidase A3	137.1	91.0	107.6	139.0	173.1	25	1.6	2.8	19	0.1	1.4	2.0	124	0.2	1.2	0.2	0.5	0.5	59.989			
208605_s_at	NM_0025292	R	8.0	1.2	4.6	9.3	8.1	0.2	0.2	0.0	0.1	0.2	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	0.0	34.7309
210258_at	AF0301071	TRK neurotrophin receptor regulator of G protein signaling (RG513)	6.2	8.4	5.6	7.1	10.9	0.3	0.1	0.4	0.5	0.5	0.0	0.1	0.3	0.1	0.0	0.0	0.2	0.3	0.0	21.7762		
207496_at	NM_0001391	R	19.9	24.7	35.4	51.9	45.6	0.9	0.1	0.5	0.3	0.1	0.1	0.5	1.8	1.6	0.5	0.7	0.9	0.4	0.3	0.2	0.3	21.1783
205857_at	AI269290		24.3	27.1	8.1	22.3	25.0	13	1.0	0.8	0.9	1.3	0.9	0.5	0.7	0.9	0.4	0.3	0.2	0.3	0.3	0.3	0.3	20.3301
210358_X_at	BC002557.1	GATA-binding protein 2	18.4	12.8	55.0	31.7	24.7	20	1.6	1.9	1.7	0.9	1.9	1.3	3.7	2.6	0.8	0.8	0.9	0.4	2.7	9.46893		
207497_s_at	D10533.1	Fepsilon R beta	10.7	28.6	34.9	12.6	6.8	15	1.0	0.8	0.8	1.9	0.9	1.7	1.5	1.7	0.7	0.7	0.7	0.3	0.5	9.39967		
203914_X_at	NM_000860.1	15-hydroxyprostaglandin dehydrogenase (PDGH) chromosome 11 open reading frame 14	63.9	51.4	24.8	36.0	23.3	4.1	4.6	4.6	2.6	1.3	0.9	1.3	1.2	6.0	1.4	1.5	0.4	0.8	0.4	6.14285		
219557_s_at	NM_020645.1		7.4	4.2	4.4	7.4	6.6	1.2	1.6	2.0	2.4	0.9	1.9	1.1	2.1	1.1	1.4	1.4	2.1	2.5	0.8	0.4	3.38029	
204061_at	NM_005044.1	protein kinase X-linked	6.2	52	52	128	169	23	27	25	24	0.8	0.4	0.7	1.2	1.9	1.5	1.5	1.5	0.4	1.6	3.26062		
202068_s_at	NM_0005272	R	24.6	16.8	16.8	9.3	28.5	13.5	1.6	1.0	1.6	0.9	0.8	2.4	1.5	2.5	2.3	2.1	3.4	3.5	0.8	0.8	0.8	3.1679

Fig. 6P

## 1. Specific transcripts markers for non-granulocytes.

Probe set	Accession #	Transcripts	MC cord	MC lung	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2 (small)	Eo 3 (small)	Eo 4 1	Ne 2 (small)	Ne 3 (small)	Ne 4 1	pI	CD4	CD8	CD14	CD19	Fb		
203547_at	U47924	CD4	5.5	4.7	2.2	1.1	1.2	2.0	1.6	0.4	0.9	0.7	1.1	0.7	0.8	3.5	15.0	0.3	17.6	1.2	0.4	
205758_at	AV006735	CD8	0.5	1.7	2.6	2.3	3.2	1.3	1.1	2.2	1.7	0.3	1.8	0.3	4.2	3.0	76.1	0.8	0.6	0.6	0.4	
206398_s_at	NM_001770.1	CD19	0.7	0.1	0.7	0.4	0.7	0.8	0.5	0.5	0.2	0.6	1.5	1.1	0.7	4.0	0.0	0.1	0.1	19.1	0.4	
211644_X_at	L14458.1	IgGV_Iregion	0.2	0.1	0.1	0.1	0.2	0.2	0.2	0.2	0.3	0.1	0.3	0.2	0.2	3.8	0.1	0.2	0.1	0.1	70.9	0.1
201743_at	NM_000591.1	CD14	18.4	2.4	0.3	0.1	0.6	8.8	0.6	1.1	3.2	40.7	49.6	58.7	68.2	2.9	0.4	0.0	97.2	1.1	0.9	
203104_at	NM_005211.1	v-fms M-CSF receptor	3.8	0.2	0.6	0.7	0.3	3.0	1.1	1.7	1.5	8.8	8.7	6.3	6.4	5.2	2.8	0.7	42.1	1.4	0.9	
209868_s_at	U63041.1	CD56	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.0	
204627_s_at	M359991.1	CD61 glycoprotein IIIa	1.7	9.4	0.2	0.1	0.3	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	48.3	0.1	0.3	0.1	0.2	0.0
216442_X_at	AK026737.1	fibronectin	0.3	1.5	0.3	0.3	0.2	0.1	1.0	0.3	0.6	0.1	0.1	0.1	0.2	0.1	0.3	0.1	1.0	0.3	0.1	92.6

Fig. 6Q

J. Raw AD levels for the median values used to normalize the raw AD levels, and the housekeeping genes.

Probe set	Accession #	Transcripts	blood	Ba 2	Ba 3	Eo	Eo	Eo 3	Eo 4	Ne	Ne	Ne 3	Ne 4					
			cord	lung	Ba 1 (small)	1	2	(small)	1	2	(small)	(small)	pl	CD4	CD8	CD14	CD19	Fb
AFIX+HSAC07/X00351_3_at	X00351	beta-actin	18334	19383	14638	20922	19151	22019	18638	21133	18568	19406	22302	16389	17569	18295	18782	20399
AFIX+HSAC07/X00351_M_at	X00351	beta-actin	22898	21777	12940	11533	7608	22560	18785	14861	13431	23106	23373	6861	8019	19368	20362	22761
AFIX+HSAC07/X00351_5_at	X00351	beta-actin	15642	15838	9516	2927	2066	17186	21061	4861	3771	18772	19768	2165	2193	14887	16381	18218
AFIX+HUMGAPDH/M33197_3_at	M33197	GAPDH	14906	13632	3640	10477	9332	2649	2844	5498	2605	2549	3186	3586	3538	5929	6429	6998
AFIX+HUMGAPDH/M33197_M_at	M33197	GAPDH	15891	16852	3218	7587	6963	2382	2565	3720	1838	2194	2796	2312	2154	6182	5931	5921
AFIX+HUMGAPDH/M33197_5_at	M33197	GAPDH	16298	16701	3479	4559	5110	1827	3121	2127	1168	2492	3476	1636	1355	4655	6826	6260
The median value of 22283 transcripts	121	1693	853	1122	1109	937	102.1	127.3	114	62.7	73.1	87.4	87.3	82.3	152.5	121.3	107.1	114.1
																		183.8

Abbreviations used in the table A-I were (small); the results obtained by the small sample protocol (see materials and methods); R: receptor; and ICN: ion channel.

**Fig. 6R**